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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:09:52 ; Search time 2151.24 Seconds  
(without alignments)  
4756.827 Million cell updates/sec

Title: US-09-724-841-1  
Perfect score: 489  
Sequence: 1 ATGAGAAATTCGAAACACCA.....TGTTCATCAACACTCTTGA 489

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:\*  
2: gb\_hgt:\*  
3: gb\_in:\*  
4: gb\_com:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_jnu:\*  
20: em\_com:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
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29: em\_vl:\*  
30: em\_hgt\_hum:\*  
31: em\_hgt\_inv:\*  
32: em\_hgt\_other:\*  
33: em\_hgtgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	489	100.0	489	5	AR004268	Sequence
2	489	100.0	489	6	AR024349	Sequence
3	489	100.0	489	6	AR070281	Sequence
4	489	100.0	489	6	AR085740	Sequence
5	489	100.0	489	6	AR122046	Sequence
6	489	100.0	489	6	AR122868	Sequence
7	489	100.0	489	6	AR125105	Sequence
8	489	100.0	489	6	AX006786	Sequence
9	489	100.0	489	6	AX320244	Sequence
10	489	100.0	489	6	I25783	Sequence
11	489	100.0	489	6	I25783	Sequence
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15	489	100.0	489	6	I25783	Sequence
16	489	100.0	489	6	I25783	Sequence
17	489	100.0	489	6	I25783	Sequence
18	487.4	99.7	489	6	BD008811	Sequence
19	487.4	99.7	489	6	BD008811	Sequence
20	482.6	98.7	489	6	AX320242	Sequence
21	481	98.4	489	6	AR094650	Sequence
22	466.6	95.4	489	6	BD008812	Sequence
23	466.6	95.4	489	6	BD008812	Sequence
24	466.6	95.4	489	6	BD008812	Sequence
25	465	95.1	489	6	AR024348	Sequence
26	465	95.1	489	6	AR070282	Sequence
27	465	95.1	489	6	AR085741	Sequence
28	465	95.1	489	6	AR122045	Sequence
29	465	95.1	489	6	AR122867	Sequence
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37	451.4	92.3	489	4	AF108148	Sequence
38	394.6	80.7	489	4	AF108148	Sequence
39	386.6	79.1	489	4	SS058142	Sequence
40	386.6	79.1	489	4	SS058142	Sequence
41	380	77.7	489	9	HS115MR1	Sequence
42	380	77.7	489	9	HS115MR2	Sequence
43	378.6	77.4	489	4	AF149700	Sequence
44	378.4	77.4	489	6	AR087004	Sequence
45	378.4	77.4	489	9	AF031167	Sequence

## ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	TITLE	JOURNAL	FEATURES	BASE COUNT	ORIGIN
1	AR004268	Sequence	4	from patent US 5747024.		Unknown.	1 (bases 1 to 489)	Grabstein, K.H. and Widmer, M.B.	Vaccine adjuvant comprising interleukin-15	Patent: US 5747024-A 4 05-MAY-1998;	159 a	79 c
	AR004268	Sequence	4	from patent US 5747024.		Unknown.	1 (bases 1 to 489)	Grabstein, K.H. and Widmer, M.B.	Vaccine adjuvant comprising interleukin-15	Patent: US 5747024-A 4 05-MAY-1998;	159 a	79 c
	AR004268	Sequence	4	from patent US 5747024.		Unknown.	1 (bases 1 to 489)	Grabstein, K.H. and Widmer, M.B.	Vaccine adjuvant comprising interleukin-15	Patent: US 5747024-A 4 05-MAY-1998;	159 a	79 c
	AR004268	Sequence	4	from patent US 5747024.		Unknown.	1 (bases 1 to 489)	Grabstein, K.H. and Widmer, M.B.	Vaccine adjuvant comprising interleukin-15	Patent: US 5747024-A 4 05-MAY-1998;	159 a	79 c
	AR004268	Sequence	4	from patent US 5747024.		Unknown.	1 (bases 1 to 489)	Grabstein, K.H. and Widmer, M.B.	Vaccine adjuvant comprising interleukin-15	Patent: US 5747024-A 4 05-MAY-1998;	159 a	79 c
	AR004268	Sequence	4	from patent US 5747024.		Unknown.	1 (bases 1 to 489)	Grabstein, K.H. and Widmer, M.B.	Vaccine adjuvant comprising interleukin-15	Patent: US 5747024-A 4 05-MAY-1998;	159 a	79 c
	AR004268	Sequence	4	from patent US 5747024.		Unknown.	1 (bases 1 to 489)	Grabstein, K.H. and Widmer, M.B.	Vaccine adjuvant comprising interleukin-15	Patent: US 5747024-A 4 05-MAY-1998;	159 a	79 c
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	AR004268	Sequence	4	from patent US 5747024.		Unknown.	1 (bases 1 to 489)	Grabstein, K.H. and Widmer, M.B.	Vaccine adjuvant comprising interleukin-15	Patent: US 5747024-A 4 05-MAY-1998;	159 a	79 c
	AR004268	Sequence	4	from patent US 5747024.		Unknown.	1 (bases 1 to 489)	Grabstein, K.H. and Widmer, M.B.	Vaccine adjuvant comprising interleukin-15	Patent: US 5747024-A 4 05-MAY-1998;	159 a	79 c
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Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DEFINITION Sequence 2 from patent US 5795966.  
 ACCESSION AR024349  
 VERSION AR024349.1 GI:3977643  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 489)  
 AUTHORS Grabstein, K.H., Pettit, D.K. and Paxton, R.J.  
 TITLE Antagonists of Interleukin-15  
 JOURNAL Patent: US 5795966-A 2 18-AUG-1998;  
 FEATURES  
 source Location/Qualifiers  
 1..489  
 BASE COUNT 159 a 79 c 95 g 156 t  
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 481 ACTTCTTGA 489  
 Db 481 ACTTCTTGA 489

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACCAATTTGAGAGTATTTCCATCCAGTGTCTACTGTGTTACTT 60  
 Db 1 ATGAGATTTCGAACCAATTTGAGAGTATTTCCATCCAGTGTCTACTGTGTTACTT 60  
 QY 61 CTAACAGTCAATTTCTAACTGAGCGATCATGTCTTCAATTTGGGCTGTTCACT 120  
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 Db 481 ACTTCTTGA 489

RESULT 3  
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 LOCUS AR070281  
 DEFINITION Sequence 1 from patent US 5892001.  
 ACCESSION AR070281  
 VERSION AR070281.1 GI:7221169  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 489)  
 AUTHORS Grabstein, K.H., Anderson, D.M., Eisenman, J.R., Fung, V. and Rauch, C.  
 TITLE Epithelium-derived T-cell factor antibodies  
 JOURNAL Patent: US 5892001-A 1 06-APR-1999;  
 FEATURES  
 source Location/Qualifiers  
 1..489  
 BASE COUNT 159 a 79 c 95 g 156 t  
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACCAATTTGAGAGTATTTCCATCCAGTGTCTACTGTGTTACTT 60  
 Db 1 ATGAGATTTCGAACCAATTTGAGAGTATTTCCATCCAGTGTCTACTGTGTTACTT 60  
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QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTAGCAAAAC 360  
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 QY 361 AGTTGCTCTTAATGGAGATGTAACAGATCTGATGCAAAAGATGAGAACTGGAG 420  
 DB 361 AGTTGCTCTTAATGGAGATGTAACAGATCTGATGCAAAAGATGAGAACTGGAG 420  
 QY 421 GAAAAAATTTAAGAAATTTTGGAGATTTGTACATATTTGCTCAATATGTCATCAAC 480  
 DB 421 GAAAAAATTTAAGAAATTTTGGAGATTTGTACATATTTGCTCAATATGTCATCAAC 480  
 QY 481 ACTTCTTGA 489  
 DB 481 ACTTCTTGA 489  
 RESULT 4 489 bp DNA linear PAT 07-SEP-2000  
 LOCUS AR085740  
 DEFINITION Sequence 1 from patent US 5985262.  
 ACCESSION AR085740  
 VERSION AR085740.1 GI:10012506  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 489)  
 AUTHORS Grabstein, K.H., Anderson, D.M., Eisenman, J.R., Fung, V. and Rauch, C.  
 TITLE Method of treatment with epithelium derived T-cell factor  
 JOURNAL Patent: US 5985262-A 1 16-NOV-1999;  
 FEATURES location/Qualifiers  
 source 1..489  
 BASE COUNT 159 a 79 c 95 g 156 t  
 ORIGIN  
 Query Match 100.0%; Score 489; DB 6; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGAGAAATTTGCAAAACCATTTTGGAGATTTTCCATCCAGTCTGCTACTGTTTACT 60  
 DB 1 ATGAGAAATTTGCAAAACCATTTTGGAGATTTTCCATCCAGTCTGCTACTGTTTACT 60  
 QY 61 CTAAACAGTATTTCTAAGTGAAGCTGGCAATCATGCTTCAATTTGGGCTGTTTCACT 120  
 DB 61 CTAAACAGTATTTCTAAGTGAAGCTGGCAATCATGCTTCAATTTGGGCTGTTTCACT 120  
 QY 121 GCAGGCTTCTTAAGCAAGAGCCCACTGGGTGAATCTTAATAGTAAATTAATTAAT 180  
 DB 121 GCAGGCTTCTTAAGCAAGAGCCCACTGGGTGAATCTTAATAGTAAATTAATTAAT 180  
 QY 181 GAAGATCTTATTCATCTATGATATGATGCTACTTATATACGAAAGTATGTTTCACT 240  
 DB 181 GAAGATCTTATTCATCTATGATATGATGCTACTTATATACGAAAGTATGTTTCACT 240  
 QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGGAGATTTCAAGTATTTTCACT 300  
 DB 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGGAGATTTCAAGTATTTTCACT 300  
 QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTAGCAAAAC 360  
 DB 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTAGCAAAAC 360  
 QY 361 AGTTGCTCTTAATGGAGATGTAACAGATCTGATGCAAAAGATGAGAACTGGAG 420  
 DB 361 AGTTGCTCTTAATGGAGATGTAACAGATCTGATGCAAAAGATGAGAACTGGAG 420  
 QY 421 GAAAAAATTTAAGAAATTTTGGAGATTTGTACATATTTGCTCAATATGTCATCAAC 480  
 DB 421 GAAAAAATTTAAGAAATTTTGGAGATTTGTACATATTTGCTCAATATGTCATCAAC 480

QY 481 ACTTCTTGA 489  
 DB 481 ACTTCTTGA 489  
 RESULT 5 489 bp DNA linear PAT 16-MAY-2001  
 LOCUS AR122046  
 DEFINITION Sequence 2 from patent US 6165466.  
 ACCESSION AR122046  
 VERSION AR122046.1 GI:14106363  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 489)  
 AUTHORS Grabstein, K.H., Pettit, D.K. and Paxton, R.J.  
 TITLE Antagonists of interleukin-15  
 JOURNAL Patent: US 6165466-A 2 26-DEC-2000;  
 FEATURES location/Qualifiers  
 source 1..489  
 BASE COUNT 159 a 79 c 95 g 156 t  
 ORIGIN  
 Query Match 100.0%; Score 489; DB 6; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATGAGAAATTTGCAAAACCATTTTGGAGATTTTCCATCCAGTCTGCTACTGTTTACT 60  
 DB 1 ATGAGAAATTTGCAAAACCATTTTGGAGATTTTCCATCCAGTCTGCTACTGTTTACT 60  
 QY 61 CTAAACAGTATTTCTAAGTGAAGCTGGCAATCATGCTTCAATTTGGGCTGTTTCACT 120  
 DB 61 CTAAACAGTATTTCTAAGTGAAGCTGGCAATCATGCTTCAATTTGGGCTGTTTCACT 120  
 QY 121 GCAGGCTTCTTAAGCAAGAGCCCACTGGGTGAATCTTAATAGTAAATTAATTAAT 180  
 DB 121 GCAGGCTTCTTAAGCAAGAGCCCACTGGGTGAATCTTAATAGTAAATTAATTAAT 180  
 QY 181 GAAGATCTTATTCATCTATGATATGATGCTACTTATATACGAAAGTATGTTTCACT 240  
 DB 181 GAAGATCTTATTCATCTATGATATGATGCTACTTATATACGAAAGTATGTTTCACT 240  
 QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGGAGATTTCAAGTATTTTCACT 300  
 DB 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTCTTGGAGATTTCAAGTATTTTCACT 300  
 QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTAGCAAAAC 360  
 DB 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTAGCAAAAC 360  
 QY 361 AGTTGCTCTTAATGGAGATGTAACAGATCTGATGCAAAAGATGAGAACTGGAG 420  
 DB 361 AGTTGCTCTTAATGGAGATGTAACAGATCTGATGCAAAAGATGAGAACTGGAG 420  
 QY 421 GAAAAAATTTAAGAAATTTTGGAGATTTGTACATATTTGCTCAATATGTCATCAAC 480  
 DB 421 GAAAAAATTTAAGAAATTTTGGAGATTTGTACATATTTGCTCAATATGTCATCAAC 480  
 QY 481 ACTTCTTGA 489  
 DB 481 ACTTCTTGA 489  
 RESULT 6 489 bp DNA linear PAT 16-MAY-2001  
 LOCUS AR122868  
 DEFINITION Sequence 2 from patent US 6168783.  
 ACCESSION AR122868

VERSION ARI22868.1 GI:14107834  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 489)  
 AUTHORS Grabslein, K.H., Pettit, D.K. and Paxton, R.J.  
 TITLE Antagonists of Interleukin-15  
 JOURNAL Patent: US 6168783-A 2 02-JAN-2001;  
 FEATURES location/Qualifiers  
 source 1..489  
 BASE COUNT 159 a 79 c 95 g 156 t  
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACATTTGAGAGATTTCCATCCAGTCTACTTGTACTT 60  
 DB 1 ATGAGATTTCGAACACATTTGAGAGATTTCCATCCAGTCTACTTGTACTT 60  
 QY 61 CTAACAGCTATTTTCTAATCTGAGCTGCATTCATCTTCAATTTGGCTGTTCACT 120  
 DB 61 CTAACAGCTATTTTCTAATCTGAGCTGCATTCATCTTCAATTTGGCTGTTCACT 120  
 QY 121 GCAGGGCTTCTTAAACAGAACGCACTGGTGATGATTAAGATTTGAAAAAATT 180  
 DB 121 GCAGGGCTTCTTAAACAGAACGCACTGGTGATGATTAAGATTTGAAAAAATT 180  
 QY 181 GAAGATCTTATTCATCTATGCAATTTGATGCTACTTTATATACGAAAGATGTTTAC 240  
 DB 181 GAAGATCTTATTCATCTATGCAATTTGATGCTACTTTATATACGAAAGATGTTTAC 240  
 QY 241 CCCAGTTGCAAGTACAGCAATGAGTCTTCTCTGGAGTTTCAAGTTATTTCACTT 300  
 DB 241 CCCAGTTGCAAGTACAGCAATGAGTCTTCTCTGGAGTTTCAAGTTATTTCACTT 300  
 QY 301 GAGTCGGAGATGCAAGTATTCATGATGCTACTTTATATACGAAAGATGTTTAC 360  
 DB 301 GAGTCGGAGATGCAAGTATTCATGATGCTACTTTATATACGAAAGATGTTTAC 360  
 QY 361 ACTTTGCTTCTAATGGAGATGATACAGATTCGATGCAAGATGAGAACTGGAG 420  
 DB 361 ACTTTGCTTCTAATGGAGATGATACAGATTCGATGCAAGATGAGAACTGGAG 420  
 QY 421 GAAAAAATTTAAAGATTTTTCAGAGTTTGTACATATTGTCCAAATGTTTCAAC 480  
 DB 421 GAAAAAATTTAAAGATTTTTCAGAGTTTGTACATATTGTCCAAATGTTTCAAC 480  
 QY 481 ACTTCTTGA 489  
 DB 481 ACTTCTTGA 489

RESULT 7  
 ARI25105 ARI25105 489 bp DNA linear PAT 16-MAY-2001  
 LOCUS Sequence 2 from patent US 6177079.  
 DEFINITION ARI25105  
 ACCESSION ARI25105  
 VERSION ARI25105.1 GI:1411167  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 489)  
 AUTHORS Grabslein, K.H., Pettit, D.K. and Paxton, R.J.  
 TITLE Antagonists of Interleukin-15  
 JOURNAL Patent: US 6177079-A 2 23-JAN-2001;  
 FEATURES location/Qualifiers  
 source 1..489

BASE COUNT 159 a 79 c 95 g 156 t  
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACATTTGAGAGATTTCCATCCAGTCTACTTGTACTT 60  
 DB 1 ATGAGATTTCGAACACATTTGAGAGATTTCCATCCAGTCTACTTGTACTT 60  
 QY 61 CTAACAGCTATTTTCTAATCTGAGCTGCATTCATCTTCAATTTGGCTGTTCACT 120  
 DB 61 CTAACAGCTATTTTCTAATCTGAGCTGCATTCATCTTCAATTTGGCTGTTCACT 120  
 QY 121 GCAGGGCTTCTTAAACAGAACGCACTGGTGATGATTAAGATTTGAAAAAATT 180  
 DB 121 GCAGGGCTTCTTAAACAGAACGCACTGGTGATGATTAAGATTTGAAAAAATT 180  
 QY 181 GAAGATCTTATTCATCTATGCAATTTGATGCTACTTTATATACGAAAGATGTTTAC 240  
 DB 181 GAAGATCTTATTCATCTATGCAATTTGATGCTACTTTATATACGAAAGATGTTTAC 240  
 QY 241 CCCAGTTGCAAGTACAGCAATGAGTCTTCTCTGGAGTTTCAAGTTATTTCACTT 300  
 DB 241 CCCAGTTGCAAGTACAGCAATGAGTCTTCTCTGGAGTTTCAAGTTATTTCACTT 300  
 QY 301 GAGTCGGAGATGCAAGTATTCATGATGCTACTTTATATACGAAAGATGTTTAC 360  
 DB 301 GAGTCGGAGATGCAAGTATTCATGATGCTACTTTATATACGAAAGATGTTTAC 360  
 QY 361 ACTTTGCTTCTAATGGAGATGATACAGATTCGATGCAAGATGAGAACTGGAG 420  
 DB 361 ACTTTGCTTCTAATGGAGATGATACAGATTCGATGCAAGATGAGAACTGGAG 420  
 QY 421 GAAAAAATTTAAAGATTTTTCAGAGTTTGTACATATTGTCCAAATGTTTCAAC 480  
 DB 421 GAAAAAATTTAAAGATTTTTCAGAGTTTGTACATATTGTCCAAATGTTTCAAC 480  
 QY 481 ACTTCTTGA 489  
 DB 481 ACTTCTTGA 489

RESULT 8  
 AX006786 AX006786 489 bp DNA linear PAT 06-SEP-2000  
 LOCUS Sequence 4 from Patent W00002582.  
 DEFINITION AX006786  
 ACCESSION AX006786  
 VERSION AX006786.1 GI:9994822  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 489)  
 AUTHORS Londel, M., Quarantino, S. and Majuri, L.  
 TITLE Treatment of celliac disease with interleukin-15 antagonists  
 JOURNAL Patent: WO 0002582-A 4 20-JAN-2000;  
 LONDEI MARCO (GB); QUARANTINO SONIA (GB); MATHILDA AND TERENCE  
 KENNEDY I (GB); MAJURI LUGI (IT)  
 FEATURES location/Qualifiers  
 source 1..489  
 BASE COUNT 159 a 79 c 95 g 156 t  
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-92;



Best Local Similarity	100.0%:	Pred No. 1,2e-92:	Mismatches	0:	Indels	0:	Gaps	0:
Matches	489:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps
OY	1	ATGAGAAATTTCCAAACACCATTTGAGAAAGTATTTCCATCCAGTGTCTACTTGTGTTACTT	60					
Db	1	ATGAGAAATTTCCAAACACCATTTGAGAAAGTATTTCCATCCAGTGTCTACTTGTGTTACTT	60					
OY	61	CTAAACAGTCATTTTCTAACTGAGCTGGCATTTCAATGTCATTTTGGGCTGTTTCACT	120					
Db	61	CTAAACAGTCATTTTCTAACTGAGCTGGCATTTCAATGTCATTTTGGGCTGTTTCACT	120					
OY	121	GCAGGGCTTCCTAAACAGAACCACTGGGTGATGTATTAAGTATTTGAAAAAAT	180					
Db	121	GCAGGGCTTCCTAAACAGAACCACTGGGTGATGTATTAAGTATTTGAAAAAAT	180					
OY	181	GAGATCTTATTCATATCTATGCAATTTGATGCTACTTTATATCCGAAGTATGTTTCAAC	240					
Db	181	GAGATCTTATTCATATCTATGCAATTTGATGCTACTTTATATCCGAAGTATGTTTCAAC	240					
OY	241	CCCAAGTTCGAAAGTAAACAGCAATGAAGTGGTTCCTCTGGAGTTACAAATTTATTTCACTT	300					
Db	241	CCCAAGTTCGAAAGTAAACAGCAATGAAGTGGTTCCTCTGGAGTTACAAATTTATTTCACTT	300					
OY	301	GAGTCCGAGATGCAAGTATTTCAATGATATACAGTACAGTAAATATCTGATCATCTTCAGAAACAC	360					
Db	301	GAGTCCGAGATGCAAGTATTTCAATGATATACAGTACAGTAAATATCTGATCATCTTCAGAAACAC	360					
OY	361	AGTTTGTCTTCTAAATGGCAATGCTAAACGAATCTGGATGCAAAAGTATGAGAACTGGAG	420					
Db	361	AGTTTGTCTTCTAAATGGCAATGCTAAACGAATCTGGATGCAAAAGTATGAGAACTGGAG	420					
OY	421	GAAGAAATATTTAAAGATTTTTCAGAGATTTTGTACATATTTGCCAAATGTTTCATCAC	480					
Db	421	GAAGAAATATTTAAAGATTTTTCAGAGATTTTGTACATATTTGCCAAATGTTTCATCAC	480					
OY	481	ACTTCTTGA 489						
Db	481	ACTTCTTGA 489						
RESULT	10							
LOCUS	125783		489 bp	DNA	linear	PAT 07-OCT-1996		
DEFINITION	Sequence 4 from patent US 5552303.							
ACCESSION	125783							
VERSION	125783.1	GI:1605653						
KEYWORDS	Unknown.							
SOURCE	Unknown.							
ORGANISM	Unclassified.							
REFERENCE	1 (bases 1 to 489)							
AUTHORS	Grabstein, K., Anderson, D., Eisenman, J., Fung, V. and Rauch, C.							
TITLE	DNA encoding epithelium-derived T-cell factor							
JOURNAL	Patent: US 5552303-A 4 03-SEP-1996;							
FEATURES	Location/Qualifiers							
source	1..489							
BASP COUNT	159 a	79 c	95 g	156 t				
ORIGIN								
Query Match	100.0%:	Score 489:	DB 6:	Length 489:				
Best Local Similarity	100.0%:	Pred. No. 1,2e-92:	Mismatches	0:	Indels	0:	Gaps	0:
Matches	489:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps
OY	1	ATGGAATTTGGAACCAATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTACTT	60					
Db	1	ATGGAATTTGGAACCAATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTACTT	60					
OY	61	CTAAACAGTCATTTTCTAACTGAGCTGGCATTTCAATGTCATTTTGGGCTGTTTCACT	120					
Db	61	CTAAACAGTCATTTTCTAACTGAGCTGGCATTTCAATGTCATTTTGGGCTGTTTCACT	120					

QY 121 GCAGGGCTTCCTAAACAGAACCCAACTGGGATGTATAAGTATTGAAAAATT 180  
DB 121 GCAGGGCTTCCTAAACAGAACCCAACTGGGATGTATAAGTATTGAAAAATT 180  
QY 181 GAAGATCTTATCAATCTATGCAATATTGATGCTACTTTATATACGAAAGATGTTCC 240  
DB 181 GAAGATCTTATCAATCTATGCAATATTGATGCTACTTTATATACGAAAGATGTTCC 240  
QY 241 CCCAGTTGCAAGATCAACAGCAATGAGTCTTCTCTGGAGTTTCAAGTTTTCACCTT 300  
DB 241 CCCAGTTGCAAGATCAACAGCAATGAGTCTTCTCTGGAGTTTCAAGTTTTCACCTT 300  
QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCCTTACCAAACTGAG 360  
DB 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCCTTACCAAACTGAG 360  
QY 361 AGTTGTCTTCTTAATGGGATGTACAGATCTGTGATGCAAAAGATGAGAACTGAG 420  
DB 361 AGTTGTCTTCTTAATGGGATGTACAGATCTGTGATGCAAAAGATGAGAACTGAG 420  
QY 421 GAAAAAATATTAAAGATTTTTCAGAGTTTGTACATATTGTCCAATGTTTCATCAG 480  
DB 421 GAAAAAATATTAAAGATTTTTCAGAGTTTGTACATATTGTCCAATGTTTCATCAG 480  
QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489  
RESULT 11  
LOCUS 128849 489 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 1 from patent US 5574138.  
ACCESSION 128849  
VERSION 128849.1 GI:1819629  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Epithelium-derived T-cell factor  
JOURNAL Patent: US 5574138-A 1 12-NOV-1996;  
FEATURES  
Location/Qualifiers  
source 1..489  
BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN  
Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1,2e-92;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCCTTACCAAACTGAG 360  
DB 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCCTTACCAAACTGAG 360  
QY 361 AGTTGTCTTCTTAATGGGATGTACAGATCTGTGATGCAAAAGATGAGAACTGAG 420  
DB 361 AGTTGTCTTCTTAATGGGATGTACAGATCTGTGATGCAAAAGATGAGAACTGAG 420  
QY 421 GAAAAAATATTAAAGATTTTTCAGAGTTTGTACATATTGTCCAATGTTTCATCAG 480  
DB 421 GAAAAAATATTAAAGATTTTTCAGAGTTTGTACATATTGTCCAATGTTTCATCAG 480  
QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489  
RESULT 12  
LOCUS 162692 489 bp DNA linear PAT 07-OCT-1997  
DEFINITION Sequence 1 from patent US 5660824.  
ACCESSION 162692  
VERSION 162692.1 GI:2480400  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Quin,L.S. and Trout,A.B.  
TITLE Muscle trophic factor  
JOURNAL Patent: US 5660824-A 1 26-AUG-1997;  
FEATURES  
Location/Qualifiers  
source 1..489  
BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN  
Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1,2e-92;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATGTCGCAAAATGTCATCAAC 480  
QY 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489

RESULT 13  
179219 179219 489 bp DNA linear PAT 10-JUN-1998  
LOCUS Sequence 1 from patent US 5707616.  
DEFINITION  
ACCESSION 179219  
VERSION 179219.1 GI:3207509  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 489)  
TITLE Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,Y. and Rauch,C.  
METHOD for treating or preventing gastrointestinal disease with  
epithelium-derived T-cell factor  
JOURNAL Patent: US 5707616-A 13-JAN-1998;  
FEATURES location/Qualifiers  
Source 1..489  
BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.2e-92;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTTTGCAGACCAATTTGAGAGTATTTCCATCCAGTCTTACTTGTACTT 60  
Db 1 ATGGAATTTTGCAGACCAATTTGAGAGTATTTCCATCCAGTCTTACTTGTACTT 60  
QY 61 CTAAACAGTCATTTTCTAATCTATGAGCTGGCATTCATGCTTCTTATTTGGCGTTTCAGT 120  
Db 61 CTAAACAGTCATTTTCTAATCTATGAGCTGGCATTCATGCTTCTTATTTGGCGTTTCAGT 120  
QY 121 GCAGGGCTTCTTAACAGCAAGCCAACTGGTGAATGTATTAAGTATTTGAAAAAAT 180  
Db 121 GCAGGGCTTCTTAACAGCAAGCCAACTGGTGAATGTATTAAGTATTTGAAAAAAT 180  
QY 181 GAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACGAAAGATGTTTCACT 240  
Db 181 GAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACGAAAGATGTTTCACT 240  
QY 241 CCCAGTTGCAAAATACAGCAATGAAGTCTTCTTGGAGTTCAGTTATTTTCACTT 300  
Db 241 CCCAGTTGCAAAATACAGCAATGAAGTCTTCTTGGAGTTCAGTTATTTTCACTT 300  
QY 301 GAGTCGGAGATGCAAGTATTCATGATAGAGTGAAGAAATCTGATCTAGCAAAACAC 360  
Db 301 GAGTCGGAGATGCAAGTATTCATGATAGAGTGAAGAAATCTGATCTAGCAAAACAC 360  
QY 361 AGTTTGTCTTCTAATGGAATGTACAGAACTGTGATGCAAAAGATGTAGAGTGGAG 420  
Db 361 AGTTTGTCTTCTAATGGAATGTACAGAACTGTGATGCAAAAGATGTAGAGTGGAG 420  
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTCAATCAAC 480  
Db 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTCAATCAAC 480  
QY 481 ACTTCTTGA 489  
Db 481 ACTTCTTGA 489

RESULT 14  
ARI03280 ARI03280 1202 bp DNA linear PAT 14-FEB-2001  
LOCUS

DEFINITION Sequence 11 from patent US 6087172.  
ACCESSION ARI03280  
VERSION ARI03280.1 GI:12814868  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 1202)  
TITLE Veerapanenl,D., Hamanaka,S. and Nozawa,I.  
JOURNAL Ribozymes targeted to human IL-15 mRNA  
PATENT: US 6087172-A 11 11-JUN-2000;  
FEATURES location/Qualifiers  
Source 1..1202  
BASE COUNT 355 a 219 c 249 g 379 t  
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 1202;  
Best Local Similarity 100.0%; Pred. No. 9.4e-93;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTTTGCAGACCAATTTGAGAGTATTTCCATCCAGTCTTACTTGTACTT 60  
Db 317 ATGGAATTTTGCAGACCAATTTGAGAGTATTTCCATCCAGTCTTACTTGTACTT 376  
QY 61 CTAAACAGTCATTTTCTAATCTATGAGCTGGCATTCATGCTTCTTATTTGGCGTTTCAGT 120  
Db 377 CTAAACAGTCATTTTCTAATCTATGAGCTGGCATTCATGCTTCTTATTTGGCGTTTCAGT 436  
QY 121 GCAGGGCTTCTTAACAGCAAGCCAACTGGTGAATGTATTAAGTATTTGAAAAAAT 180  
Db 437 GCAGGGCTTCTTAACAGCAAGCCAACTGGTGAATGTATTAAGTATTTGAAAAAAT 496  
QY 181 GAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACGAAAGATGTTTCACT 240  
Db 497 GAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACGAAAGATGTTTCACT 556  
QY 241 CCCAGTTGCAAAATACAGCAATGAAGTCTTCTTGGAGTTTCAAGTATTTTCACTT 300  
Db 557 CCCAGTTGCAAAATACAGCAATGAAGTCTTCTTGGAGTTTCAAGTATTTTCACTT 616  
QY 301 GAGTCGGAGATGCAAGTATTCATGATAGAGTGAAGAAATCTGATCTAGCAAAACAC 360  
Db 617 GAGTCGGAGATGCAAGTATTCATGATAGAGTGAAGAAATCTGATCTAGCAAAACAC 676  
QY 617 GAGTCGGAGATGCAAGTATTCATGATAGAGTGAAGAAATCTGATCTAGCAAAACAC 676  
QY 677 AGTTTGTCTTCTAATGGAATGTACAGAACTGTGATGCAAAAGATGTAGAGTGGAG 736  
Db 677 AGTTTGTCTTCTAATGGAATGTACAGAACTGTGATGCAAAAGATGTAGAGTGGAG 736  
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCAATCAAC 480  
Db 737 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCAATCAAC 796  
QY 481 ACTTCTTGA 489  
Db 797 ACTTCTTGA 805

RESULT 15  
AX024715 AX024715 1202 bp DNA linear PAT 15-SEP-2000  
LOCUS Sequence 1 from Patent W00028019.  
DEFINITION  
ACCESSION AX024715  
VERSION AX024715.1 GI:10184794  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1202)  
AUTHORS Doudevani,A. and Chaimovitz,C.  
TITLE Antisense oligomer

## JOURNAL

Patent: WO 0028019-A 1 18-MAY-2000;  
MOR RESEARCH APPLIC LTD (IL) ; DOUDEVANI AMOS (IL) ; UNIV BEN  
GURION (IL) ; CHAIMOVITZ CIDIO (IL)

FEATURES  
source  
1. 1202  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 355 a 219 c 249 g 379 t  
ORIGIN

## Query Match

Best Local Similarity 100.0%; Score 489; DB 6; Length 1202;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGACAAATTCGAACACCAATTTGGAGATATTCACATCCAGTGTACTTGTGTTACTT 60
Db 317 ATGAGAAATTCGAACACCAATTTGGAGATATTCACATCCAGTGTACTTGTGTTACTT 376
QY 61 CTAACACAGTCATTTTCTAAGCTGAGCTGCATGCTCATTTTGGCTGTTTCACT 120
Db 377 CTAACACAGTCATTTTCTAAGCTGAGCTGCATGCTCATTTTGGCTGTTTCACT 436
QY 121 GCAGGGCTTCTTAACAGAGCCCACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 180
Db 437 GCAGGGCTTCTTAACAGAGCCCACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 496
QY 181 GAAGATCTTATTCATCTATGCAATTTGAGCTACTTTATATACGAAAGTGAATGTTTCA 240
Db 497 GAAGATCTTATTCATCTATGCAATTTGAGCTACTTTATATACGAAAGTGAATGTTTCA 556
QY 241 CCCAGTTGCAAGATGACAGCAATGAAGTCTTCTCTTGGAGTTTACAAAGTTATTTCACTT 300
Db 557 CCCAGTTGCAAGATGACAGCAATGAAGTCTTCTCTTGGAGTTTACAAAGTTATTTCACTT 616
QY 301 GAGTCCGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTAGCAACAAAC 360
Db 617 GAGTCCGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTAGCAACAAAC 676
QY 361 AGTTTGCTCTTAATGGAGATGTAACAGAACTGATGCAAGAAATGTGAGAACTGAG 420
Db 677 AGTTTGCTCTTAATGGAGATGTAACAGAACTGATGCAAGAAATGTGAGAACTGAG 736
QY 421 GAAAAAAATTTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAATGTTCAATCAAC 480
Db 737 GAAAAAAATTTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAATGTTCAATCAAC 796
QY 481 ACTTCTTGA 489
Db 797 ACTTCTTGA 805
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Search completed: June 19, 2002, 01:32:22  
Job time: 4950 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:09:42 ; Search time 254.13 Seconds  
(without alignments)  
3303.707 Million cell updates/sec

Title: US-09-724-841-1  
Perfect score: 489  
Sequence: 1 ATGAGAAATTTCGAAACCA.....TGTCATCAACACTTCTTGA 489

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

1: N\_Geneseq\_032802.\*  
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.\*  
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
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25: /SIDSL1/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	489	100.0	489	16	AA00526
2	489	100.0	489	16	AA084584
3	489	100.0	489	17	AA049455
4	489	100.0	489	17	AA042243
5	489	100.0	489	17	AA036635
6	489	100.0	489	18	AA058404
7	489	100.0	489	19	AA023554
8	489	100.0	489	19	AA02873
9	489	100.0	489	20	AA029479

10	489	100.0	489	21	AA090032	Human interleukin-15
11	489	100.0	489	21	AA038244	Simian epithelium-Simian interleukin-15
12	489	100.0	489	22	AA014655	Simian ERF (SEPF)
13	489	100.0	489	22	AA057017	Human IL-15 (DNA)
14	489	100.0	1202	20	AA056368	Human low adenosin
15	489	100.0	1202	21	AA021342	Human interleukin-15
16	489	100.0	1202	21	AA058044	Human adenosine re
17	489	100.0	1202	21	AA055220	Human IL-15 cDNA
18	489	100.0	1202	21	AA0288708	Human low adenosin
19	489	100.0	17904	21	AA021345	Wild-type interlev
20	487.4	99.7	489	18	AA097227	Mutant interleukin
21	481	98.4	489	18	AA097228	Simian interleukin
22	465	95.1	489	16	AA00524	Simian IL-15 clone
23	465	95.1	489	17	AA084583	Human epithelium d
24	465	95.1	489	17	AA049456	Simian interleukin
25	465	95.1	489	17	AA042242	Human epithelium d
26	465	95.1	489	17	AA036634	Human epithelium d
27	465	95.1	489	19	AA02874	Human ERF (HEPF) p
28	465	95.1	489	20	AA029480	Human epithelium d
29	465	95.1	489	21	AA090031	Human ERF (HEPF) p
30	465	95.1	489	21	AA038245	Human adenosine re
31	465	95.1	489	22	AA057018	Human low adenosin
32	385	78.7	17844	21	AA035223	Human adenosine re
33	378.4	77.4	1248	21	AA021341	Human interleukin
34	378.4	77.4	1248	21	AA035219	Human low adenosin
35	378.4	77.4	1248	21	AA021344	Human adenosine re
36	351.6	71.9	486	21	AA021344	Human interleukin
37	351.6	71.9	486	21	AA035222	Simian ERF (SEPF)
38	345	70.6	345	16	AA00527	Simian interleukin
39	345	70.6	345	16	AA057024	Human ERF (HEPF) m
40	325.8	66.6	345	16	AA00525	Human low adenosin
41	325.8	66.6	345	22	AA057025	Human adenosine re
42	141.6	29.0	14968	21	AA021343	Human IL-15 gene a
43	141.6	29.0	14968	21	AA035221	Human interleukin
44	141.6	29.0	14968	22	AA014664	
45	141.6	29.0	14968	22	AA015838	

## ALIGNMENTS

RESULT 1	
AA00526	AA00526 standard; cDNA; 489 BP.
ID	AA00526
XX	AA00526
AC	02-FEB-1996 (first entry)
XX	
DT	Human interleukin-15 precursor.
DE	Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.
XX	
KW	Homo sapiens.
OS	
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..489
FT	/*tag= a
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FT	145..489
FT	/*tag= b
FT	/note= "claimed"
XX	
PN	WO9527722-A.
PD	19-OCT-1995.
PF	06-APR-1994; 94WO-US03793.
PR	06-APR-1994; 94WO-US03793.
PA	(IMMV ) IMMUNEX CORP.
XX	

PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
PI Rauch C;

DR WPI: 1995-373556/48.  
DR P-PSDB: AAR83438.

PT Isolated DNA encoding polypeptide with mammalian IL-15 activity - which  
PT stimulates proliferation and differentiation of T cells, used for  
PT treating carcinoma(s), melanomas, etc. and viral infections

PS Claim 36: Page 28-29; 48pp: English.

CC A simian species of IL-15 (sIL-15) was purified and its AA  
CC sequence and cDNA sequence analysed (see AAR83309, AAR83436,  
CC AAR00524, AAR00525). Both the simian and the human ORFs encode  
CC a precursor polypeptide (AAR83436, AAR83438). The precursor  
CC polypeptides each comprise a 48-AA leader sequence and a sequence  
CC encoding mature simian or human IL-15 polypeptides. The active  
CC simian and human IL-15 polypeptides are disclosed in AAR83309 &  
CC AAR83438. The invention also comprises other mammalian  
CC IL-15, including human IL-15, that hybridise to probes defined by  
CC AAR83438. A plasmid contg. a recombinant clone of human IL-15  
CC cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 69245.  
CC The deposit was named 141-hETF. AAR83435 is a mammalian mature  
CC IL-15 polypeptide. It is a generic sequence which encompasses both  
CC AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.  
CC XX

SO Sequence 489 BP: 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 16; Length 489;  
Best Local Similarity 100.0%; Pred. No. 5.7e-117;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACCACTTTGAGAAGTATTTCCATCCAGTGTACTGTTACTT 60  
DB 1 atgagaatttcgaacacacattgagaagatttcacacagtcacttggttactt 60  
QY 61 CTAAGAGTCATTTTCTTAAGTGAAGTGCATCATGCTCTTCAATTTGGGCTGTTCACT 120  
DB 61 ctaaacagtcatttcttaactgaagctgcacatcgtcttcaatttggcctgttcaagt 120  
QY 121 GCAGGCTTCTTAAGACAGCAACTGGTGAATGTAATAGTATTTGAAAAAAT 180  
DB 121 gcaggcttccttaaacagacacactggtgaatgataagatttgaaaaaat 180  
QY 181 GAAGATCTTATTCATCTATGCATATGATGCTACTTTATATACGAAAGTATGTTAC 240  
DB 181 gaagatcttataatcctatgcatatgtacttataacgaaagtgatgttcaac 240  
QY 241 CCCAGTTGCAAAAGTAACAGCAATGAAGTCTTCTTGAGATTACAGTTATTTCACTT 300  
DB 241 cccagttgcaaaagtaacagcaatgaagtgcttctcttggaattacaagttatttcaact 300  
QY 301 GAGTCGGAGATGCAAGTATTTATCATACAGTAGAAAAATCTGATCATCTAGCAAAAC 360  
DB 301 gagtcggagatgcaagtatTTATCATACAGTAGAAAAATCTGATCATCTAGCAAAAC 360  
QY 361 AGTTTGCTTCTTAAGGAAATGTACAGAAATCTGATGCAAAAGAAATGTGAGAACTGGAG 420  
DB 361 agtttgcttcttaaggaatgtacagaaatctggaatgcaaaagaaatgtgagaaactggaag 420  
QY 421 GAAAAAATATTTAAAGATTTTTCAGAGTGTGTTGATATTTGCAAAATTTGATCAAC 480  
DB 421 gaaaaaataataaagaatttctgcaagttcttgacatattgcacaaatgttatacaac 480  
QY 481 ACTTCTTGA 489  
DB 481 acttcttga 489

RESULT 2  
AA084584

ID AA084584 standard; cDNA; 489 BP.

AC AA084584;

DT 04-SEP-1995 (first entry)

DE Human IL-15 clone 141.hETF.

XX Interleukin-15; IL-15; hIL-15; T-cell growth factor;

KM antitumor; viricide; ss.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 1..489 /tag= a

FT sig\_peptide 1..144 /product= IL-15 precursor

FT mat\_peptide 145..486 /tag= b

FT /tag= c /product= mature IL-15

PN ZA9402636-A.

PD 28-DEC-1994.

PF 18-APR-1994; 942A-0002636.

PR 18-APR-1994; 942A-0002636.

PA (IMV) IMMUNEX CORP.

PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;

PI Rauch C;

DR WPI: 1995-082473/11.

DR P-PSDB: AAR66927.

PT New purified interleukin-15 - which induces T cell proliferation

PT and differentiation, used for the treatment of tumours and viral

PT infection

PS Disclosure: Page 28-29; 47pp: English.

CC A sIL-15 probe was prepared from isolated simian interleukin-15

CC cDNA and used to screen a cDNA library generated from the IMPLH

CC cell line derived from human bone marrow stromal cells. Clone

XX 141.hETF encoded human IL-15.

SO Sequence 489 BP: 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 16; Length 489;  
Best Local Similarity 100.0%; Pred. No. 5.7e-117;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACCACTTTGAGAAGTATTTCCATCCAGTGTACTGTTACTT 60  
DB 1 atgagaatttcgaacacacattgagaagatttcacacagtcacttggttactt 60  
QY 61 CTAAGAGTCATTTTCTTAAGTGAAGTGCATCATGCTCTTCAATTTGGGCTGTTCACT 120  
DB 61 ctaaacagtcatttcttaactgaagctgcacatcgtcttcaatttggcctgttcaagt 120  
QY 121 GCAGGCTTCTTAAGACAGCAACTGGTGAATGTAATAGTATTTGAAAAAAT 180  
DB 121 gcaggcttccttaaacagacacactggtgaatgataagatttgaaaaaat 180  
QY 181 GAAGATCTTATTCATCTATGCATATGATGCTACTTTATATACGAAAGTATGTTAC 240  
DB 181 gaagatcttataatcctatgcatatgtacttataacgaaagtgatgttcaac 240

OY 241 CCCAGTGCAGAACTACAGCAATGAGTCTTCTCTGAGTTACAGTTATTCATT 300  
 DB 241 cccagtgcaaaagtacacgaatgaagtgcttctcttgagttacaaagtattcaatt 300  
 OY 301 GAGTCCGAGATGACAGTATTCATGATACAGTAAATCTGATCTAGCAAAACAC 360  
 DB 301 gagtcgagatgcaagatctcatgatacagtagaaatctgatactccgaacaacac 360  
 OY 361 AGTTGTCTCTTAATGAGATGACAGATGATGCAAAAGATGTGAGCACTGGAG 420  
 DB 361 agttgtctcttaagtgaatgaacagatctgatacagtagaaatctgagaaatcggag 420  
 OY 421 GAAAAAATATTAAGCAATTTTGCAGAGTTTGTACATATTTCCAAATGTCATCAAC 480  
 DB 421 gaaaaaatattcaagaattttgcagagtttgtacatatgtccaaatgttccaaac 480  
 OY 481 ACTTCTTGA 489  
 DB 481 acttcttga 489  
 RESULT 3  
 AAT49455  
 ID AAT49455 standard; cDNA; 489 BP.  
 AC AAT49455;  
 XX  
 DT 11-MAR-1997 (first entry)  
 DE Simian epithelium derived T cell factor cDNA.  
 XX  
 KM SETF: African green monkey; CV1/EBNA cell; T-cell; B-cell;  
 KM lymphocyte; proliferation; differentiation; gastrointestinal;  
 KM HIV infection; human immunodeficiency virus; ss.  
 XX  
 OS Cercopithecus aethiops.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..489  
 FT mat\_peptide 145..486  
 FT /\*tag= a  
 FT /\*tag= b  
 FT /product= SETF  
 XX  
 PN USS574138-A.  
 PD 12-NOV-1996.  
 XX  
 PF 08-MAR-1993; 93US-0031399.  
 XX  
 PR 22-FEB-1995; 95US-0393305.  
 PR 08-MAR-1993; 93US-0031399.  
 PR 22-APR-1994; 94US-0233606.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
 PI Rauch C;  
 DR WPI; 1996-517923/51.  
 DR P-PSDB; AAM09098 AND AAM09099.  
 XX  
 PT New epithelium derived T cell factor - induces proliferation of T  
 PT and B cells; stimulates destruction of tumour and virus infected  
 PT cells and protects against toxicity, partic. for treating intestinal  
 PT disease and HIV infection  
 XX  
 PS Claim 1; Fig 1; 35pp; English.  
 CC The simian ETF (epithelium derived T cell factor) was isolated from  
 CC African green monkey CV1/EBNA cell conditioned medium. The N-  
 CC terminal sequence of the purified SETF was determined and then PCR  
 CC primers were designed based on the sequence information. A 92 bp

CC Fragment was amplified from CV1/EBNA DNA and was used as a probe to  
 CC screen a CV1/EBNA cDNA library for the full-length SETF coding  
 CC sequence (i.e. the present sequence). Mature SETF induces  
 CC proliferation and/or differentiation of precursor or mature T cells  
 CC and is useful for promoting long-term in vitro culture of  
 CC T-lymphocytes and T-cell lines. It is used for treating  
 CC gastrointestinal diseases including peptic ulcer, colitis and  
 CC malignancy and for treating HIV infection.  
 XX  
 SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;  
 Query Match 100.0%; Score 489; DB 17; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 ATGAGAAATTTGGAACCAATTTGAGAGATTTCCATCCAGTCTTGTGTTACTT 60  
 DB 1 atgagaatttcgaaccacattgagaagtattccaccagtgctacttggttactt 60  
 OY 61 CTAAACAGCATTTTCTAATGAGAGTGGATGATGATGATTTGGGCTGTTCACT 120  
 DB 61 ctaaacagcatcttcttaactgaagctggaatcagatcttcaatcttgaggcttccagt 120  
 OY 121 GCAGGCTTCTCTAAGACAGACCACTGGGTGATGATTAATAGTGAATTTGAAAAAT 180  
 DB 121 gcaggcttctcttaaaacagaagccaactgggtgagtgaatgaatgttgaaaaaatt 180  
 OY 181 GAAGATCTTATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 DB 181 gaagatcttattcaatctatcagatgacttacttataataagaaatgagatgctaac 240  
 OY 241 CCCAGTGCAGAACTACAGCAATGAGTCTTCTCTGAGTTACAGTTATTCATT 300  
 DB 241 cccagtgcaaaagtacacgaatgaagtgcttctcttgagttacaaagtattcaatt 300  
 OY 301 GAGTCCGAGATGACAGTATTCATGATACAGTAAATCTGATCTAGCAAAACAC 360  
 DB 301 gagtcgagatgcaagatctcatgatacagtagaaatctgatactccgaacaacac 360  
 OY 361 AGTTGTCTCTTAATGAGATGACAGATGATGCAAAAGATGTGAGCACTGGAG 420  
 DB 361 agttgtctcttaagtgaatgaacagatctgatacagtagaaatctgagaaatcggag 420  
 OY 421 GAAAAAATATTAAGCAATTTTGCAGAGTTTGTACATATTTCCAAATGTCATCAAC 480  
 DB 421 gaaaaaatattcaagaattttgcagagtttgtacatatgtccaaatgttccaaac 480  
 OY 481 ACTTCTTGA 489  
 DB 481 acttcttga 489  
 RESULT 4  
 AAT42243  
 ID AAT42243 standard; DNA; 489 BP.  
 AC AAT42243;  
 XX  
 DT 05-FEB-1997 (first entry)  
 DE Human epithelium-derived T cell factor gene.  
 XX  
 KM Epithelium-derived T-cell factor; simian; human; culture; proliferation;  
 KM epithelial cell; differentiation; T-lymphocyte; African green monkey;  
 KM primer; PCR; polymerase chain reaction; amplification; probe; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..144  
 FT mat\_peptide 145..486





OY	241	CCACTTCCGAAGTAACAGCATGAAGTGCCTTCTCTGTGAGTTACAGTTATTTCACTT	300
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OY	301	GAGTCCGAGAGTAAGTAATTTTCATGATACAGTAGAAGAAATCTGATCCTCAGCAAAAC	360
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OY	361	AGTTTGCTCTTCAATGCGAATGTATACAGAAATCTGATGCAAGAAATGTGAGAACTGGAG	420
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OY	421	GAAAAAAATATTAAGAAATTTTTCGACAGTTTGTCAATATGTGCCAAATGTCATCAAC	480
Db	421	gaaaaaaatattaagaatcttgcagagcttctgacatatgtgccaaatgttcatcaac	480
OY	481	ACTTCTTGA 489	
Db	481	actctctga 489	
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AAAT58404			
ID	AAAT58404	standard; cDNA; 489 BP.	
XX	AAAT58404;		
AC			
DT	18-MAR-1997	(first entry)	
XX			
DE		Interleukin-15 coding sequence.	
XX			
KW	IL-15; interleukin-15; T-cell growth factor; proliferation; stimulate;		
KM	muscle growth; differentiation; hypertrophy; treat; atrophy; wasting;		
KW	skeletal; cardiac; muscle; congestive heart failure; diabetes-associated;		
XX	glucose-intolerance; dyslipidaemia; rhabdomyosarcoma; dystrophy; ss.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..489	
FT		/tag= a	
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XX			
PN	W09637223-A1.		
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PD	28-NOV-1996.		
XX			
PF	07-MAY-1996;	96WO-US06423.	
XX			
PR	24-MAY-1995;	95US-0535733.	
XX			
PA	(IMMAY ) IMMUNEX CORP.		
XX			
PI	Grabstein KH, Quinlan LS, Troutt AB;		
XX			
DR	WPI; 1997-020939/02.		
XX	P-PsDB; AAM01658.		
PT	Muscle trophic compsn. contg. interleukin 15 - for treating, e.g.		
XX	congestive heart failure, muscle wasting etc.		
PS			
XX	Disclosure; Page 12; 22pp; English.		
CC	This sequence encodes human interleukin-15 (IL-15) (see AAM01658), a		
CC	known T-cell growth factor that can support proliferation of an		
CC	IL-2-dependent cell line, CTL-2. Compsns. contg. IL-15 to stimulate		
CC	muscle growth, differentiation or hypertrophy are claimed. The		
CC	stimulation of muscle growth is useful for treating atrophy, or wasting,		
CC	in particular, skeletal and cardiac muscle atrophy. The compsn. further		
CC	comprises a steroid, growth hormone and insulin-like growth factor.		
CC	Congestive heart failure, muscle wasting and diabetes-associated		
CC	glucose-intolerance or dyslipidaemia, rhabdomyosarcoma and muscular		

CC dystrophy can all be treated by such comps..  
XX  
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match	100.0%;	Score 489;	DB 18;	Length 489;
Best Local Similarity	100.0%;	Pred. No. 5.7e-117;		
Matches 489;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGAGATTTTGGAAACCAACATTTTAGAAGATTTCCATCCAGGCTACCTGGTTACTT	60
Db	1	atggaattctgaaacacacatttgaagaattatccatccagtgctacttvgtttaactt	60
QY	61	CTAAACACTCATTTTCTPACGTAAGAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTCA	120
Db	61	ctaaacagtcattcttaacctgaagctggcatctatgtcttcatttctggcttgcttcagt	120
QY	121	GCAGGCGTTCCTTAAACAGAAAGCCAACTGGGTGAATGTAATAGCTATTTGAAAAAATT	180
Db	121	gcagggcttccctaaacacgaagcccaactcgggtgaatgtaataagtgattcgaaaaaatt	180
QY	181	GAAAGATCTTATTCATCTATGCAATATTGATGCTCTTATATACGGAAGATGATTTAC	240
Db	181	gaagatcttatccaactcctaigcatatgatlgtactcttatatacgaagaatgtagttcac	240
QY	241	CCCAGTTCCAAAGTATACAGCAATGAAGGCTTCTCCTTGGAGTACAAAGTTATTTCACTT	300
Db	241	cccagttccaagtaacacgcaatgaaggcttccctcttggaagtacaaagtatttcaactc	300
QY	301	GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAAAAATCGATCATCTTAGCAAAACAC	360
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Db	361	agtttgctcttcaatggaatctglaacaaacatctgattgcaagaagtgtgaagaactggag	420
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QY	481	ACTTCTTGA 489	
Db	481	acttcttga 489	

RESULT	7
ID	AAV23554
AC	AAV23554 standard; cDNA; 489 bp.
DT	13-JUL-1998 (first entry)
DE	Human interleukin-15 coding sequence.
XX	
XX	
XX	Human; interleukin-15; IL-15; T cell; B cell; proliferation; vaccine
KW	cytokine; growth factor; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
CDS	1..489
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PN	US5747024-A.
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PD	05-MAY-1998.
XX	
PF	19-JUN-1995; 95US-0504042.
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PR	19-JUL-1995; 95US-0504042.
PR	08-MAR-1993; 93US-0033399.

PR 22-APR-1994; 94US-0233606.  
 PR 22-FEB-1995; 95US-0393305.  
 XX  
 PA (IMV ) IMMUNEX CORP.  
 XX  
 PI Grabstein KH, Widmer MB,  
 XX  
 DR WPI, 1998-285678/25.  
 DR P-PSDB; AAW53878.  
 XX  
 PT Use of Interleukin-15 - to enhance immunogenicity of a vaccine  
 XX  
 PS Disclosure: Column 5-6; 5pp; English.

CC This sequence encodes human interleukin-15 (IL-15), which can be used in  
 CC the vaccine of the invention. The vaccine composition comprises an  
 CC immunogenic amount of a vaccine antigen (Ag) and an  
 CC immunogenicity-augmenting amount of IL-15. The composition is useful for  
 CC enhancing the immunogenicity of a vaccine. The cytokine IL-15 is a potent  
 CC T and B cell growth factor. It causes proliferation and differentiation  
 CC of these cells and augments T cell mediated immune responses. The vaccine  
 CC composition can sufficiently elicit an immune response without being  
 CC deleterious to the recipient, especially when using pathogenically  
 CC deficient antigens. Some vaccines do not elicit a strong immune response  
 CC and cannot provide sufficient protection on further exposure to the  
 CC antigen.  
 CC  
 XX  
 XX

Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 19; Length 489;  
 Best Local Similarity: 100.0%; Pred. No. 5,7e-117;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACCATTTGAGAGTATTTCCATCCAGTGGTACTGTTTACTT 60  
 Db 1 atgagaatttcgaacaccatttgagaagtatttcaccacagtgctacttggttactt 60  
 QY 61 CTAAACAGTCAATTTCTTACTGAGCTGGCATTCATGCTCTTCAATTTGGCGTGTTCAGT 120  
 Db 61 ctaaacagtcatttcttaactgaagctgcatctcatctctcatttggtcgttccagt 120  
 QY 121 GCAGGGCTTCTTAAACAGACCCCACTGGGTGATGTAATTAAGTATTGAAAAAATT 180  
 Db 121 gcagggtcttccaaacaggaagccaactggctgaatgaatgaattgaaaaaatt 180  
 QY 181 GAAGATCTTATTCATATCATATGATGCTACTTATATACGAAAGATGTTTAC 240  
 Db 181 gaagatcttattcaatcatcatgcatatttgactacttatacogaaagatgttcaac 240  
 QY 241 CCCAGTTGCAAGTAACGCAATGAAGCTTTCTCTTGAGATTACAAAGTTATTTGACTT 300  
 Db 241 cccagttgcaagtaacgcaatgaagcttctctctgtgagttacaagttatttccatt 300  
 QY 301 GAGTCGCGAGATGCAAGTATTCATGATGATAGTAATAATCGATCAGCAAAACAC 360  
 Db 301 gagtcgcgagatgcaagatattcatgatacagtaagaataccgacatccctagcaaacac 360  
 QY 361 AGTTGCTCTTCTTAATGGGAATGTAAAGAAATCTGATGCAAAAGATGTAGAGACTGGAG 420  
 Db 361 agttgctcttcttaattgggaatgtaaagaaatctgatacgaatgtgagaaactggag 420  
 QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTATCAAC 480  
 Db 421 gaaaaaataattaaagaattttgcagagttttgtacatattgccaatgttcatcaaac 480  
 QY 481 ACTTCTTGA 489  
 Db 481 acttcttga 489

RESULT 8  
 AAV02873

ID AAV02873 standard; DNA; 489 BP.  
 AC AAV02873;  
 XX  
 DT 08-MAY-1998 (first entry)  
 XX  
 DE Simian epithelium derived T-cell factor DNA.  
 KW Epithelium derived T-cell factor; ERF; simian; gastrointestinal disease;  
 KW B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;  
 KW treatment; prevention; ss.  
 XX  
 OS Simian.

Key	Location/Qualifiers
CDS	1..489
sig_peptide	/*tag= a 1..48
mat_peptide	/*tag= b 49..486
/*tag= c	
/product= ERF	
/note= "Epithelium-derived T-cell factor"	

US5707616-A.  
 13-JAN-1998.  
 04-OCT-1996; 96US-0726817.  
 22-FEB-1995; 95US-0393305.  
 08-MAR-1993; 93US-0031399.  
 22-APR-1994; 94US-0233606.

(IMV ) IMMUNEX CORP.  
 Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
 PI Rauch C;  
 DR WPI: 1998-100295/09.  
 DR P-PSDB; AAW39185.

Treatment or prevention of gastrointestinal diseases - by  
 administering epithelium-derived T-cell factor polypeptide  
 Claim 1C: Column 35-36; 34pp; English.

CC This sequence encodes a simian epithelium-derived T-cell factor (ERF)  
 CC which is used in a method for treating or preventing gastrointestinal  
 CC disease. These polypeptides have particular application in the treatment  
 CC of gastrointestinal disorders associated with disruption of the  
 CC gastrointestinal epithelium or villi such as chemotherapy- and  
 CC radiation-therapy induced enteritis (gut toxicity), mucositis, peptic  
 CC ulcer disease, gastroenteritis and colitis, villus atrophic disorders,  
 CC malignancy and inflammatory bowel disease. ERF polypeptides may also be  
 CC useful in the treatment of human immunodeficiency virus (HIV) and  
 CC HIV-associated disease due to their ability to stimulate CD4+ and CD8+  
 CC cells. Biologically active ERF may be used to treat a variety of other  
 CC diseases or conditions where T-cell or B cell stimulation is desired.  
 CC  
 XX  
 XX

Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 19; Length 489;  
 Best Local Similarity: 100.0%; Pred. No. 5,7e-117;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACCATTTGAGAGTATTTCCATCCAGTGGTACTGTTTACTT 60  
 Db 1 atgagaatttcgaacaccatttgagaagtatttcaccacagtgctacttggttactt 60  
 QY 61 CTAAACAGTCAATTTCTTACTGAGCTGGCATTCATGCTCTTCAATTTGGCGTGTTCAGT 120  
 Db 61 ctaaacagtcatttcttaactgaagctggcatTTATGCTCTTCAATTTGGCGTGTTCAGT 120

Db	61	ctaacagctcaattcttctaacggaagctgacatcatgctctcaatttgggcgttcaagt	120
Oy	121	GCAGGCGTTCCCTAAACAGAAAGCCAACTGGGTGAATGTATATAGTATTGAAAAAATT	180
Db	121	gcagggtcttccctaaacagaagccacctgaggctgaatgaataaagttcgtaaaaaaatc	180
Oy	181	GAAGATCTTATTCATCATCATGATATGATGATGCTACTCTTATATATACGAAGAATGATGTTCAC	240
Db	181	gaagctcttatctcaatccatgcatctatgctctactcttatataacggaagaatgattcacc	240
Oy	241	CCCACTTGCAAAGTAAACAGACAAATGAAGTGCCTTCTCTTGGAGTTACAAATTATTTCACTT	300
Db	241	cccagctgcaaaagtacacagcaatgagcttctctcttggagttacaagttcttccact	300
Oy	301	GAGTCCGGAGATGCAGATTCATCATCATGATGATGAGAAATTCGATCATCTCTACCAAAACAC	360
Db	301	gagtcctgagagagcaagatcttcaatgatacagaagaataatctgatactcccaagaacaac	360
Oy	361	AGTTTGCTTCTTAATGGAGATGTAAACAGAAATCGATGCCAAAGAAATGTGAGAACTGGAG	420
Db	361	agtttgctcttctcaatgaggaaatgtaacagaatctgagtgaagaatgtaggaactggag	420
Oy	421	GAATAAATATTAAGCATTTTTCGAGAGTTTGTACATATTCGTCAAATGTTCAATCAAC	480
Db	421	gaaaaaatattaaagaattttgcagaggtttgtacatcatctgcctcaaatgttccatcaac	480
Oy	481	ACTTCTTGA 489	
Db	481	acttcttga 489	
RESULT	9		
AAx29479			
ID	AAx29479	standard; DNA; 489 BP.	
XX	AAx29479;		
AC			
DT	10-JUN-1999	(first entry)	
DE		Simian epithelium-derived T-cell factor (ETF) encoding DNA.	
XX			
KW		Epithelium-derived T-cell factor; ETF; immunoassay; enteritis; ulcer;	
KW		T cell proliferation; gastrointestinal disease; mucositis; colitis;	
KW		gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease;	
KW		human immune deficiency virus; tumour; simian; ss.	
XX			
OS	Mammalia.		
XX			
PN	US5892001-A.		
XX			
PD	06-APR-1999.		
XX			
PF	04-OCT-1996;	96US-0725969.	
XX			
XX	22-FEB-1995;	95US-0393305.	
PR	08-MAR-1993;	93US-0031399.	
PR	22-APR-1994;	94US-0233606.	
XX	04-OCT-1996;	96US-0725969.	
XX			
PA	(IMMV ) IMMUNEX CORP.		
XX			
PI	Anderson DM, Eisenman JR, Fung V, Grabstein KH;		
PI	Rauch C;		
XX			
DR	WPI, 1999-253930/21.		
XX	P-PsDB; AAY03756, AAY03757.		
PT	Antibodies specific for epithelium-derived T-cell growth factor		
XX			
PS	Claim 1; Columns 35-36; 34pp. English.		
XX			
CC	The invention relates to an isolated antibody that binds specifically to a simian or human epithelium-derived T-cell factor (ETF) polypeptide. The		

CC	antibodies are used, optionally when immobilized or labeled, to detect
CC	and quantify E7F in standard immunoassays. They may also be used as
CC	diagnostic and therapeutic agents, e.g. when conjugated to toxins (or
CC	their precursors) or radionuclides. E7F induces proliferation and/or
CC	differentiation of T cells (or their precursors), e.g. for use in
CC	establishing long term in vitro cultures; and is also used to treat
CC	gastrointestinal disease (e.g. enteritis or mucositis induced by
CC	chemotherapy or radiation, peptic ulcer, gastroenteritis, colitis,
CC	villus atrophy, malignancy and inflammatory bowel disease), to treat
CC	human immune deficiency virus infection or associated disease, or
CC	generally in any situation requiring stimulation of T or B cell
CC	proliferation, secretion of immunoglobulins or certain cytokines,
CC	increased anti-infection disease immunity, induction of T-cell lytic
CC	activity or increased destruction of tumour or virus-infected cells. The
CC	present sequence represents a DNA encoding a simian E7F precursor
XX	polypeptide sequence.
SO	
Sequence	489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;
Query Match	100.0%; Score 489; DB 20; Length 489;
Best Local Similarity	100.0%; Pred. No. 5.7e-117;
Matches	489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ATGAGATTTCCAACCACTTGGAGAATATTTCATCCAGTGCGACTGTGGTTACTT 60
DB	1 attgagatttcgaacacatcttgaaagcatcaccacccagtgctaacttggttacct 60
OY	61 CTAAACAGTCATTTTTCTTAACCTGAAGCTGCATCATCATCTTCAATTTTGGCTGTTCAGT 120
DB	61 ctaaacagcatctttcttaactcgaagtgcatacctcaatcttcaatttggcgcttcagt 120
OY	121 GCAGGCGTTCTTAAACACAGGCCAAGCTGGTGATGTATAAGTATTTGAAAAAATT 180
DB	121 gcagggtcttcctaaacaagaagccaacttgggtgaatgtaaatgatattgaaaaaat 180
OY	181 GAAGATCTTATTCATCTATTCATATGATATGATGCTTATATACGGAAGTAGTGTTCAC 240
DB	181 gaagatcttatcctaactctatgcatactgataugcaattatacgcgaagtagtctcac 240
OY	241 CCCAGTGTCAAAGTAAACACAATGAAGTGCCTTCTCTTGAGACTTACAAATTATTTCACTT 300
DB	241 ccagtggtcaaagtaaacaagaatgaagtgccttctctcttgagfllaacaagttattcact 300
OY	301 GAGTCGGAGATGCAGATATTATGATPACAGTAGAATAATCTGTATCCTTAGCAAACAC 360
DB	301 gagtcggagatgcaagatcatactgatacagtagaaaatctgataccttaagcaaacac 360
OY	361 AGTTTCTCTCTTAATGSGAATGTAACAGAAATCGAATGCAAAAAGTGGAGAACTGGAG 420
DB	361 agtttctctcttaatgggaatgtaacagaatcggaatgcaaaaagtggaagactggag 420
OY	421 GAAAAAAATTAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
DB	421 gaaaaaaaaatatgaagaattttgcagagtttgttacataatgtccaatgttcatcaac 480
OY	481 ACPTCTTGA 489
DB	481 actctctga 489
RESULT	10
ID	AAZ90032
XX	AAZ90032 standard; cDNA; 489 BP.
XX	AAZ90032;
DT	09-MAY-2000 (first entry)
DE	Human interleukin-15 (IL-15) nucleotide sequence.
XX	Interleukin-15; IL-15; antagonist; irritable bowel disease; IBD;
KM	celiac disease; treatment; human; ss.

XX OS Homo sapiens.  
 XX PN MO200002582-A2.  
 XX PD 20-JAN-2000.  
 XX PF 09-JUL-1999; 99WO-GB02201.  
 XX PR 10-JUL-1998; 98GB-0014892.  
 XX PA (KENN-) KENNEDY INST RHEUMATOLOGY MATHILDA & TER.  
 XX PI Londei M, Quarantino S, Mairi L;  
 XX DR WPI: 2000-171080/15.  
 XX P-PSDB: AAY78595.  
 XX PT Use of antagonists of Interleukin-15 for treating an inflammatory bowel  
 XX PS disease, particularly celiac disease  
 XX CC Disclosure: Page 70; 70pp; English.  
 CC This sequence represents the human Interleukin 15 (IL-15) nucleotide  
 CC sequence. The IL-15 nucleotide sequence and the protein encoded by it can  
 CC be used to determine and create antagonists of IL-15. An antagonist of  
 CC IL-15 can be used for treating an inflammatory bowel disease (IBD). The  
 CC invention relates to the treatment of celiac disease using IL-15  
 CC antagonists. The antagonists are preferably mutants of IL-15, antibodies  
 CC against IL-15 or IL-15 molecules bound to chemical groups that interfere  
 CC with the ability of IL-15 to effect a signal transduction through either  
 CC the alpha or the gamma subunit of the IL-15 receptor complex. The IL-15  
 CC antagonists of the invention can be used to treat irritable bow disease  
 CC especially celiac disease.  
 XX SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 21; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 5,7e-117;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACACATTTGGAAGTATTTCCATCCAGCTGCTACTGTTTACTT 60  
 Db 1 atgagaatttcgaacacacatttggaagtattttccatccagctgctactggtttactt 60  
 QY 61 CTAAACAGTCAATTTCTTACTGTAAGCTGCAATTCATGCTCTCATTTGGCGTTCAGT 120  
 Db 61 ctaaacagtcaatttcttactgaagctgcaatTCATGCTCTCATTTGGCGTTCAGT 120  
 QY 121 GCAGGCTTCTTAAGACGAAGCACTGGGTGAATGTAATAGTATTGAAAAAATT 180  
 Db 121 gcaggcttcttaagacgaagccactgggtgaatgtaatagtattgaaaaaatt 180  
 QY 181 GAAGATCTTATTCATCATGATATGATGCTTACTTATATACGGAAGAGATGTTTAC 240  
 Db 181 gaagatcttattcatcatgatacgaatgcttacttataatacgaagaagatggtttac 240  
 QY 241 CCCAGTTGCAAGTAACAGCAATGAGTCTTCTCTTGAGATTACAGTATTATTTCACTT 300  
 Db 241 cccagttgcaagtaacagcaatgagcttctcttgagattacagattatttcaactt 300  
 QY 301 GAGTCCGGAGATGCAAGTATTCATGATGACGTAGAAAAATCTGATCATTAGCAACAC 360  
 Db 301 gagtccggagatgcaagtattcatgatacagtagaaaaatcgtacatccctagaacaac 360  
 QY 361 AGTTGCTTCTTAATGGGAATGTAACAGAAATCTGATGCAAGAAATGAGAGACTGAG 420  
 Db 361 agttgcttcttaatgggaatgtaacagaaatctgatacgaagaatgtagagactgag 420  
 QY 421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTGCAAAATGTTGATCAAC 480  
 Db 421 gaaaaaataatlaagaatttttcagagtttgtacatattgccaanaatgattcataac 480

QY 481 ACTTCTTGA 489  
 Db 481 acttcttga 489

RESULT 11  
 AA238244  
 ID AA238244 standard; cDNA; 489 BP.  
 AC AA238244;  
 XX 09-FEB-2000 (first entry)  
 DE Simian epithelium-derived T-cell factor (ETF) cDNA.  
 KW ETF; epithelium-derived T-cell factor; T-cell; T-lymphocyte;  
 KW proliferation; differentiation; growth factor; precursor; mature; CD4+;  
 KW CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;  
 KW gastrointestinal disease; gastroenteritis; colitis;  
 KW inflammatory bowel disease; villus atrophic disorder; enteritis;  
 KW chemotherapy; radiotherapy; gut toxicity; cancer; side effect;  
 KW tolerated dose; ss.  
 OS Mammalia.  
 XX Key Location/Qualifiers  
 FH CDS 1..489  
 FT /\*tag- a  
 FT /\*product= "Simian ETF precursor protein (AA238244)"  
 FT 1..144  
 FT /\*tag- b  
 FT mat\_peptide 145..489  
 FT /\*tag- c  
 FT /\*product= "Mature simian ETF (AA238244)"  
 FT US5985262-A.  
 XX 16-NOV-1999.  
 XX 03-FEB-1997; 97US-0794524.  
 XX 22-FEB-1995; 95US-0393305.  
 PR 04-OCT-1996; 96US-0726817.  
 PR 08-MAR-1993; 93US-0031399.  
 PR 22-APR-1994; 94US-0233606.  
 XX (IMMEX ) IMMUNEX CORP.  
 PI Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;  
 XX WPI: 2000-022267/02.  
 DR P-PSDB: AAY52308, AAY52309.  
 PT Stimulation of T-cells in human immunodeficiency virus infected  
 PT patients -  
 XX Claim 1; Columns 35-36; 33pp; English.  
 PS This sequence represents simian epithelium-derived T-cell factor (ETF)  
 CC cDNA. ETF is a previously unidentified T-cell growth factor which  
 CC stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to proliferate  
 CC and differentiate. It also promotes proliferation of the gastrointestinal  
 CC epithelium. The protein can be used to promote long-term in vitro culture  
 CC of T-lymphocytes and T-cell lines. ETF can be used for treating HIV  
 CC infection, HIV-associated diseases, and other diseases or conditions  
 CC where stimulation of T-cell proliferation would be desirable e.g., it  
 CC could be used to augment the destruction of tumour cells or virally-  
 CC infected cells. ETF may also be used to treat or prevent gastrointestinal  
 CC disease, including chemotherapy and radiotherapy associated enteritis,  
 CC gastroenteritis, colitis, inflammatory bowel disease and villus atrophic  
 CC disorders. Chemotherapy and radiotherapy associated enteritis (gut  
 CC toxicity) results in bleeding and sepsis due to gastrointestinal flora

CC entering the blood, and thus can limit the dosage of therapeutic agent  
 CC administered to a cancer patient. EPF may therefore be used to increase  
 CC the tolerated doses radiotherapy and chemotherapy.

XX Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 21; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACCACTTTGAGAGATTTCCATCCAGCGCTACTGTGTACTT 60  
 1 atgagaatttcgaacacacatttgagaagatttcacacagtcactgttcttactt 60  
 Db 61 CTAACAGCTATTTCTCAATGAGCGATGCTTCTTCAATTTGGCTGTTCACT 120  
 61 ctaaacagctatttcctcaacagcctgcattcacttcttcttcttcttcttctt 120  
 Db 61 ctaaacagctatttcctcaacagcctgcattcacttcttcttcttcttcttctt 120  
 QY 121 GCAAGGCTTCTTAACAGACCACTGGGTGAATGAATGAATGAATGAATGAAT 180  
 121 gcaaggcttcttaaacagacccaactgggtgaatgaaatgaaatgaaatgaaat 180  
 Db 121 gcaaggcttcttaaacagacccaactgggtgaatgaaatgaaatgaaatgaaat 180  
 QY 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 181 gaagatcttattcatctatctatctatctatctatctatctatctatctatctat 240  
 Db 181 gaagatcttattcatctatctatctatctatctatctatctatctatctatctat 240  
 QY 241 CCCAGTTGCAAGATGACAGCAATGAGTGTCTTCTTCTTCTTCTTCTTCTTCTT 300  
 241 cccagttgcaagatgacagcaatgagtgtcttcttcttcttcttcttcttcttctt 300  
 Db 241 cccagttgcaagatgacagcaatgagtgtcttcttcttcttcttcttcttcttctt 300  
 QY 301 GAGTCGGAGATGCAAGTATTCATGATGATGATGATGATGATGATGATGATGATGAT 360  
 301 gagtcggagatgcaagatgattcagatgatacagaaatcgcattcctcagcaaac 360  
 Db 301 gagtcggagatgcaagatgattcagatgatacagaaatcgcattcctcagcaaac 360  
 QY 361 AGTTGCTTCTTAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 420  
 361 agttgcttcttaaatggaaatggaaatggaaatggaaatggaaatggaaatggaaat 420  
 Db 361 agttgcttcttaaatggaaatggaaatggaaatggaaatggaaatggaaatggaaat 420  
 QY 421 GAAAAAATATTAAGAAATTTTTCAGAGTTTGTATCATATTTGCCAATGTCATCAAC 480  
 421 gaaaaaataatataagaatttttgcagagtttgcataatgttcacaaatgttcacaa 480  
 Db 421 gaaaaaataatataagaatttttgcagagtttgcataatgttcacaaatgttcacaa 480  
 QY 481 ACTTCTTGA 489  
 481 acttcttga 489  
 Db 481 acttcttga 489

RESULT 12  
 AAD14465  
 ID AAD14465 standard; DNA; 489 BP.

XX AAD14465;  
 AC 15-NOV-2001 (first entry)  
 DT Human interleukin 15 (IL-15) DNA coding sequence.  
 DE Human interleukin 15; IL-15; gene therapy; chromosome 4q31; infection;  
 XX Human; interleukin 15; IL-15; gene therapy; chromosome 4q31; infection;  
 KW drug screening; anthropological lineage; paternity testing; HIV;  
 KW Human immunodeficiency Virus; forensic application; T-cell leukemia; ds.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..489  
 FT /tag= a  
 FT /product= "Human IL-15 protein"  
 XX  
 XX WO200158914-A2.  
 XX  
 XX 16-AUG-2001.  
 XX

PF 08-FEB-2001; 2001WO-US04130.

XX 08-FEB-2000; 2000US-0181059.

XX (GENA-) GENAISSANCE PHARM INC.

PI Anastasio AE, Chew A, Denton RR, Nandabalan K, Stephens JC;

DR WPI: 2001-522460/57.

DR P-PSDB: AAE08576.

PT Novel polynucleotides comprising one of 11, PSI-PS11, single nucleotide  
 PT polymorphisms in human interleukin-15 gene, and useful for treating  
 PT disorders affected by expression of function of interleukin-15 isogene

Dislosure; Fig 2; 78pp; English.

The present sequence is human interleukin-15 (IL-15) DNA coding sequence  
 located on chromosome 4q31. The polymorphic variants of IL-15 genes are  
 useful for studying the expression and function of IL-15 and expressing  
 IL-15 protein for use in screening for candidate drugs to treat diseases  
 related to IL-15 activity. Genotyping or haplotyping an individual at the  
 novel IL-15 polymorphic sites are useful for studying population  
 diversity, anthropological lineage, the significance of diversity and  
 lineage of the phenotypic level, paternity testing, forensic applications  
 and for identifying associations between IL-15 genetic variation and a  
 trait such as level of drug response or susceptibility to disease.  
 Identifying an association between a genotype or haplotype and a trait,  
 identifying an association between diagnostic tests and therapeutic treatments for  
 CC infections, human immunodeficiency virus and T-cell leukemia. The  
 CC identification of an association between a clinical response and a  
 CC genotype or haplotype (or haplotype pair) for the IL-15 gene may be the  
 CC basis for designing a diagnostic method to determine those individuals  
 CC who will or will not respond to the treatment, or alternatively, will  
 CC respond at a lower level and thus may require more treatment, i.e. a  
 CC greater dose of a drug. The genotyping or haplotyping methods are also  
 CC useful for developing drugs targeting IL-15. The genotyping and  
 CC haplotyping methods are also useful in designing clinical trials. IL-15  
 CC DNA is useful for therapeutic purposes for treating disorders affected  
 CC by expression of function of novel IL-15 isogene and also in gene  
 CC therapy. Expression of an IL-15 isogene may be turned off by transforming  
 CC a targeted organ, tissue or cell population of an expression vector  
 CC that expresses high levels of untranslated mRNA for the isogene.

Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 22; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-117;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACCACTTTGAGAGATTTCCATCCAGCGCTACTGTGTACTT 60  
 1 atgagaatttcgaacacacatttgagaagatttcacacagtcactgttcttactt 60  
 Db 1 atgagaatttcgaacacacatttgagaagatttcacacagtcactgttcttactt 60  
 QY 61 CTAACAGCTATTTCTCAATGAGCGATGCTTCTTCTTCTTCTTCTTCTTCTT 120  
 61 ctaaacagctatttcctcaacagcctgcattcacttcttcttcttcttcttcttctt 120  
 Db 61 ctaaacagctatttcctcaacagcctgcattcacttcttcttcttcttcttcttctt 120  
 QY 121 GCAAGGCTTCTTAACAGACCACTGGGTGAATGAATGAATGAATGAATGAAT 180  
 121 gcaaggcttcttaaacagacccaactgggtgaatgaaatgaaatgaaatgaaat 180  
 Db 121 gcaaggcttcttaaacagacccaactgggtgaatgaaatgaaatgaaatgaaat 180  
 QY 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 181 gaagatcttattcatctatctatctatctatctatctatctatctatctatctat 240  
 Db 181 gaagatcttattcatctatctatctatctatctatctatctatctatctatctat 240  
 QY 241 CCCAGTTGCAAGATGACAGCAATGAGTGTCTTCTTCTTCTTCTTCTTCTTCTT 300  
 241 cccagttgcaagatgacagcaatgagtgtcttcttcttcttcttcttcttcttctt 300  
 Db 241 cccagttgcaagatgacagcaatgagtgtcttcttcttcttcttcttcttcttctt 300  
 QY 301 GAGTCGGAGATGCAAGTATTCATGATGATGATGATGATGATGATGATGATGATGAT 360

inflammatory bowel disease; for increasing tolerated doses for radiation therapy and chemotherapy agents which are limited by gastrointestinal toxicity; and for treating HIV and HIV-associated diseases. The antibodies are further used to treat a variety of other diseases or conditions where it is desired to stimulate proliferation of T-lymphocytes, to augment anti-infectious disease immunity, to induce CTL, LAK or NK lytic activity, or to augment the destruction of tumour cells or cells infected with virus. The present sequence represents a cDNA encoding the simian ERF (SERF) polypeptide.

Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

er;

89;

Q.

9

XX 29-OCT-1998; 98MO-IB01837.  
 XX 31-OCT-1997; 97US-0962503.  
 XX (HISM ) HISAMITSU PHARM CO LTD.  
 XX Hamanaka S, Nozawa I, Veerapeneni D;  
 XX WPI, 1999-313334/26.  
 XX  
 XX New ribozymes targeted to interleukin-15 mRNA  
 XX  
 XX Disclosure; Fig 8; 46pp; English.  
 XX  
 XX The present sequence describes an isolated RNA molecule which  
 XX specifically cleaves mRNA encoding interleukin 15 (IL-15). The  
 XX enzymatic RNA molecules can bind to and cleave mRNA encoding IL-15.  
 XX They can be used for treating disorders associated with IL-15 such  
 XX as inflammatory disorders, e.g. rheumatoid arthritis by inhibiting  
 XX the synthesis of IL-15 in lymphocytes and preventing the recruitment  
 XX and activation of macrophages. They can also be used to develop  
 XX transgenic animals which can be used to identify the impact of  
 XX increased or decreased IL-15 levels on a particular pathway or  
 XX phenotype. The present sequence represents a human IL-15 DNA sequence.  
 XX  
 XX Sequence 1202 BP; 355 A; 219 C; 249 G; 379 T; 0 other;

Query Match 100.0%; Score 489; DB 20; Length 1202;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-117;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGAGAAATTTGGAACACATTTGAGAAGTATTTCCATCCAGTGTGCTTACTT 60  
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 DB 317 atgagatttcgaaccacattgagaagatttcacacagtgctactgtgttactt 376  
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 QY 61 CTAAACAGTCATTTTCTACTGAAAGTGCATTCATGCTCTTCACTTTGGCTGTTTCAGT 120  
 |||||||  
 DB 377 cttaaaagtcatttcttaactgaagctgacatcattgcttcaatcttggcgttcaagt 436  
 |||||||  
 QY 121 GCAGGCTTCTCTAAACAGAACCCAACTGGGTGAATGTAATAGTGAATTTGAAAAAATT 180  
 |||||||  
 DB 437 gcaaggcttccctaacaacagacgaactgggaagtaagtaagtgattgaaaaaatt 496  
 |||||||  
 QY 181 GAAGATCTTATTCATCTATGATGATTTGATGCTACTTTATATACGGAAGTGAATGTTTAC 240  
 |||||||  
 DB 497 gaagatcttcaatcattgaatgatgactacttatacgaagtgatgttcac 556  
 |||||||  
 QY 241 CCAGTTCGAAAGTAACAGCAATGAAGTGTCTTCTTGAGATTACAAAGTTATTTCCTT 300  
 |||||||  
 DB 557 cccagttgcaaaagtaacagaatgaagtgcttctctcttgagtaacaaagttatttccct 616  
 |||||||  
 QY 301 GAGTCGAGATCCAAAGTATTCATGATAGTGAATGATGATCATCTAGCAAAAC 360  
 |||||||  
 DB 617 gacgcggagatgcaagatcattcatgatacagtagaaatctgataccccaagaacaaac 676  
 |||||||  
 QY 361 AGTTTGTCTTCTAATGGGAATGTAACAGAAATCTGGATGCAAAAGATGTGAGAG 420  
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 DB 677 agttgtcttctaattggaatgtaacagaatctgatacgaagaatgtggaactggaag 736  
 |||||||  
 QY 421 GAAAAAAATTTTAAAGAAATTTTGAGAGTTTGTACATTTTGCCAAAGTTCATCAAC 480  
 |||||||  
 DB 737 gaaaaaaataataagaattctgcagagttctgtacataatgtccaaatgttataaac 796  
 |||||||  
 QY 481 ACTTCTTGA 489  
 |||||||  
 DB 797 acttcttga 805

RESULT 15  
 AAF21342  
 ID AAF21342 standard; DNA: 1202 BP.

XX AAF21342;  
 AC 14-MAR-2001 (first entry)  
 XX  
 XX Human low adenosine antisense oligonucleotide related sequence #2909.  
 DE  
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiallergic; hypotensive; cytotatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200062736-A2.  
 PN  
 XX 26-OCT-2000.  
 PD  
 XX 24-MAR-2000; 2000MO-US08020.  
 PF  
 XX 06-APR-1999; 99US-0127958.  
 PR  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA (NYCE/) NYCE J W.  
 XX  
 XX Nyce JW;  
 PI  
 XX WPI; 2000-679539/66.  
 DR  
 XX  
 XX Low adenosine (A) content antisense oligonucleotides which do not  
 PT trigger adenosine receptors during metabolism, useful e.g. for treating  
 PT cancers and respiratory obstructions -  
 PS  
 XX Disclosure; Page 1344-1345; 1592pp; English.  
 XX  
 XX The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiallergic, hypotensive and cytotatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and/or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC transmitters, defenses, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergies  
 CC and/or surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention.  
 XX  
 XX Sequence 1202 BP; 355 A; 219 C; 249 G; 379 T; 0 other;

Query Match	100.0%	Score 489;	DB 21;	Length 1202;
Best Local Similarity	100.0%	Pred. No. 7,2e-117;		
Matches	489;	Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0;
QY	1	ATGACAATTTCGAAACCCACATTTGGGAAGATTTTCCATCCACAGCTGCTACTTGTGTTTACTT	60	
Db	317	atgagaaatttcgaaaccacatttggaaagtatttccaccagttgactcttgyttactt	376	
QY	61	CTAAACAGTGCATATTTCTTAACCTGACCTGGCATATGATCTTCATTTTGGGGCTTTCGT	120	
Db	377	ctaaacagtcatttcttcaactcgaagcttgcattcaatgcttccattcttggcctgttccagt	436	
QY	121	GCAGGGCTTCCTTAAACAGAACCCAACTGGGTGAATGTAATAGTATTGAAAAAAATT	180	
Db	437	gcaggcttccctaaacagaagccaactcggltgaaatgtaaatgaagatttgaaaaaaatt	496	
QY	181	GAAGATCTTATTTCATCTATGCATATTGATGCTACTTTATATACGGAAGTGATGTTTAC	240	
Db	497	gaagctctattccaactatcatgatacttgaatgctactattatatacggaaagatgttccac	556	
QY	241	CCCATTTTCCAAAGTAAACAGCAATGAAAGGGCTTTCCTTGGAATTGCAAGTTATTTCACTT	300	
Db	557	cccgatttgcagaatgatacagcaatgaagtgcttctctcttggaggttacaagttatttccatt	616	
QY	301	GAGTCGCGAGATGCAAGTATTTCAATGATACAGTACAAAAATCGATCATCTGACAAACAC	360	
Db	617	gagtcggaagatgcagatattcattcatgatatagtagaanaattcgatcatctctagcaaacac	676	
QY	361	AGTTTGCTTCTAATGGGAATGTAACAGAACTGTGATGCCAAGAANTGTGAGCAACTGGAG	420	
Db	677	agtttgcttcttcaatgggaatgtaacagaatcttgaatgcagaagaatttggagaaacttggag	736	
QY	421	GAAAAAAATATTTAAAGATTTTTCACAGATTTTGTGACATTTATGTCACAAATGTCATCAC	480	
Db	737	gaaaaaaatattaaagaatttcttcagaggttcttgaactatgttccaaaatgttcaatcac	796	
QY	481	ACTTCTTCA 489		
Db	797	acttcttca 805		

Search completed: June 19, 2002, 00:56:15  
Job time: 2793 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2002, 23:04:52 ; Search time 2237.54 Seconds  
(without alignments)  
2949.673 Million cell updates/sec

Title: US-09-724-841-1

Perfect score: 489  
Sequence: 1 ATGAGAAATTTCGAACACCACA.....TGTTCATCAACACTTCTTGA 489

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlmu:\*  
5: em\_estlov:\*  
6: em\_estlpl:\*  
7: em\_estlro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	489	100.0	982	AL548180	AL548180 AL548180
2	430.2	88.0	994	AL572832	AL572832 AL572832
3	399.4	81.7	509	AA463370	AA463370 ZX87d12.r
4	348.8	71.3	800	BG184658	BG184658 RST3720.A
5	295.8	60.5	637	AI186008	AI186008 wnt2903.x
6	292	59.7	756	BI832895	BI832895 6030824240
7	244	49.9	872	BI758686	BI758686 603024240
8	210.6	43.1	826	BI685688	BI685688 60309529
9	176.2	36.0	309	BF095213	BF095213 t12-UT007
10	174	35.6	471	N76741	N76741 yz82912.r1
11	166.6	34.1	690	AI596704	AI596704 vk38h11.y
12	152.8	31.2	474	N49734	N49734 yz06b12.s1
13	150.2	30.7	538	AI152482	AI152482 u683d09.r
14	150	30.3	515	BF704348	BF704348 MI-P-O3-a
15	148.2	28.5	564	AA863763	AA863763 vx08d07.r
16	139.6	28.5	631	BB661271	BB661271 BB661271
17	132.4	27.1	166	BF379349	BF379349 RC2-UT002

18	116	23.7	181	9	AA497102	AA497102 ae32d05.r
19	107.2	21.9	817	10	BI756810	BI756810 603024487
20	106.2	21.7	590	9	AA544966	AA544966 vk38h11.r
21	105.8	21.6	488	9	BB825167	BB825167 BB825167
22	103.2	21.1	430	9	AA858936	AA858936 UT-R-A0-a
23	98.2	20.1	420	10	BE690327	BE690327 u66b02.y
24	90	18.4	550	10	BE698667	BE698667 RC2-UT002
25	87.6	17.9	429	9	AA863979	AA863979 vx87e05.r
26	86.2	17.6	648	9	AA874636	AA874636 vx81e08.r
27	86	17.0	718	10	BI766231	BI766231 603052877
28	83	17.0	434	9	AI503616	AI503616 vx38h12.x
29	82	16.8	494	9	AA804168	AA804168 PM4-UM008
30	75.6	15.5	405	9	AA121368	AA121368 UT-M-BR2
31	75.4	15.4	301	10	BF088290	BF088290 CM1-HT087
32	74.4	15.2	509	9	AI120615	AI120615 uc28h10.r
33	73.8	15.1	275	10	BF088272	BF088272 CM1-HT087
34	72	14.7	483	9	AA804165	AA804165 PM4-UM008
35	56	11.5	391	12	AZ334843	AZ334843 IM0064H21
36	55.8	11.4	278	9	BE177883	BE177883 RC3-HT060
37	49.8	10.2	987	12	CNS014PQ	AL104456 Drosophila
38	44	9.0	1101	12	CNS0039G	AL063921 Drosophila
39	43.2	8.8	740	10	BM167297	BM167297 EST569820
40	43	8.8	1310	12	CNS0152W	AL106118 Drosophila
41	42.4	8.7	1204	12	CNS016E2	AL063247 Drosophila
42	42.2	8.6	1101	12	CNS000M2	AL108171 Drosophila
43	42	8.6	1010	12	CNS017KX	AL438101 T3 end of
44	41.2	8.4	1010	12	CNS07BNJ	AL438101 T3 end of
45	41	8.4	998	12	CNS00L0Z	AL067831 Drosophila

#### ALIGNMENTS

RESULT 1  
AL548180  
LOCUS AL548180 LTI\_NFL006.PL2 982 bp mRNA linear EST 16-FEB-2001  
DEFINITION AL548180 LTI\_NFL006.PL2 Homo sapiens cDNA clone CS00D1034Y009 5  
prime, mRNA sequence.  
ACCESSION AL548180  
VERSION AL548180.1 GI:12882943  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 982)  
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.

#### FEATURES

source

1. 982  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS00D1034Y009"  
/clone\_id="LTI\_NFL006.PL2"  
/tissue\_type="placenta"  
/note="Vector: PCWSPORT 6; Site\_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end was enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCWSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA fax : (1) 301 610 8371  
Email : fliang@lifestech.com URL :  
http://fulllength.invitrogen.com 1 others  
BASE COUNT 275 a 208 c 214 g 284 t  
ORIGIN

Query Match 100.0%; Score 489; DB 9; Length 982;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-104; Mismatches 0; Indels 0; Gaps 0;  
 Matches 489; Conservative 0;

1 ATGAGATTTCGAACCACTTTGAGAGTATTTCCATCCAGTGTACTGTGTACTT 60  
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 358 ATGAGATTTCGAACCACTTTGAGAGTATTTCCATCCAGTGTACTGTGTACTT 417  
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 61 CTAAAGCATTTTCTAAGTGAAGTGCATCATCTTCTTATTTGGCGTGTTCAGT 120  
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 418 CTAAAGCATTTTCTAAGTGAAGTGCATCATCTTCTTATTTGGCGTGTTCAGT 477  
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 478 GCAGGCTTCTTAAACAGAGCAACTGGGTGAATGATTAAGTATTTGAAAAAAT 537  
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 181 GAAGATCTTATTCATCTATGATATGATGCTACTTATTAAGCAAGATGATTTGAC 240  
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 538 GAAGATCTTATTCATCTATGATATGATGCTACTTATTAAGCAAGATGATTTGAC 597  
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 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTTCTTGGAGTTTCAAGTTTTCACCT 300  
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 598 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTTCTTGGAGTTTCAAGTTTTCACCT 657  
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 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTACCAAAACAC 360  
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 658 GAGTCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTACCAAAACAC 717  
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 361 ACTTTGCTTCTTAAAGGGAATGTAACAGAAATGATGCAAAAGATGTGAGAACTGAG 420  
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 718 ACTTTGCTTCTTAAAGGGAATGTAACAGAAATGATGCAAAAGATGTGAGAACTGAG 777  
 |||||||  
 421 GAAAAAATATTTAAAGATTTTTCAGAGTTTGTACATATTTGCAATGTTTCATCAAC 480  
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 778 GAAAAAATATTTAAAGATTTTTCAGAGTTTGTACATATTTGCAATGTTTCATCAAC 837  
 |||||||  
 481 ACTTCTGA 489  
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 838 ACTTCTGA 846

RESULT 2 994 bp mRNA linear EST 16-FEB-2001  
 AL572832/c LOCUS  
 DEFINITION AL572832 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CS0D1034Y009 3  
 prime, mRNA sequence.  
 ACCESSION AL572832  
 VERSION AL572832  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 994)  
 AUTHORS Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
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 1. 994  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
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 /issue\_type="placenta"  
 /note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-stranded cDNA was digested with Not I and  
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by  
 Life Technologies. Contact : Feng Liang Life Technologies,  
 a division of Invitrogen 9800 Medical Center Drive  
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
 Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com"  
 BASE COUNT 333 a 186 c 154 g 316 t 5 others  
 ORIGIN

Query Match 88.0%; Score 430 2; DB 9; Length 994;  
 Best Local Similarity 98.6%; Pred. No. 1e-90; Mismatches 2; Indels 0; Gaps 0;  
 Matches 429; Conservative 4;

55 TTACTTCTAAACAGCATTTTCTAAGTGAAGTGCATCATCTTCTTATTTGGGCTGT 114  
 |||||||  
 994 TTACTTCTAAACAGCATTTTCTAAGTGAAGTGCATCATCTTCTTATTTGGGCTGT 935  
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 115 TTCACTGAGGCTTCTTAAACAGAGCAACTGGGTGAATGATTAAGTATTTGAAA 174  
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 934 TTCACTGAGGCTTCTTAAACAGAGCAACTGGGTGAATGATTAAGTATTTGAAA 875  
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 175 AAAATTGAAGATCTTATTCATCTATGATATGATGCTACTTATTAAGCAAGTAT 234  
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 235 GTTACCCCACTTGCAGAAAGTAAACAGCAATGAAGTCTTCTTCTTGAAGTTAAT 294  
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 814 GTTACCCCACTTGCAGAAAGTAAACAGCAATGAAGTCTTCTTCTTGAAGTTAAT 755  
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 295 TCACCTTGAGTCCGAGATGCAAGTATTCATGATGATGATGATGATGATGATGATGAT 354  
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 754 TCACCTTGAGTCCGAGATGCAAGTATTCATGATGATGATGATGATGATGATGATGAT 695  
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 355 AACCAAGTTTGTCTTCTAATGAGGATGTAAACAGATCTGATGCAAAAGATGTGAGAA 414  
 |||||||  
 694 AACCAAGTTTGTCTTCTAATGAGGATGTAAACAGATCTGATGCAAAAGATGTGAGAA 635  
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 415 CTGAGGAGAAAAAATATTTAAAGATTTTTCAGAGTTTGTACATATTTGCCAAATGTTG 474  
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 634 CTGAGGAGAAAAAATATTTAAAGATTTTTCAGAGTTTGTACATATTTGCCAAATGTTG 575  
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 475 ATCAACACTTCTTGA 489  
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 574 ATCAACACTTCTTGA 560

RESULT 3 509 bp mRNA linear EST 10-JUN-1997  
 AA463370 LOCUS  
 DEFINITION AA463370 zx97d12.r1 Soares, Nihmpu, SI Homo sapiens cDNA clone IMAGE:811703 5,  
 similar to SW:IL15\_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ;, mRNA  
 sequence.  
 ACCESSION AA463370  
 VERSION AA463370  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 509)  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,  
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Merra, M., Martin, J., Moore, B.,  
 Schellenberg, K., Stepien, M., Tan, F., Thelsting, B., White, Y., Wyllie,  
 T., Waterston, R., and Wilson, R.  
 TITLE Washu-Merck EST Project 1997  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: estelw@wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone; similarity on wrong strand. Seq primer: -28m13 rev2 Et from Amersham. High quality sequence stop: 416.

## FEATURES

## SOURCE

1. 509  
/organism="Homo sapiens"  
/db\_xref="GDB:6042614"  
/db\_xref="taxon:9606"  
/clone="IMAGE:811703"  
/clone\_lib="Scarses\_NbHMPu.S1"  
/tissue\_type="Pooled human melanocyte, fetal heart, and pregnant uterus"  
/lab\_host="DH10B"  
/note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI. Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHM, pregnant uterus NBHPU, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT  
ORIGIN

149 a 91 c 108 g 161 t

Query Match 81.7%; Score 399.4; DB 9; Length 509;  
Best Local Similarity 99.8%; Pred. No. 1.6e-83;  
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAATTCGAAACACATTTGAGAAGTATTCATCCAGTGCCTACTTGTCTTACTT 60  
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DB 105 ATGGAATTCGAAACACATTTGAGAAGTATTCATCCAGTGCCTACTTGTCTTACTT 164  
QY 61 CTAAACAGTATTTCTTAACTGAAGTGGCATTCATCTTCACTTTGGCTGTTTCACT 120  
|||||  
DB 165 CTAAACAGTATTTCTTAACTGAAGTGGCATTCATCTTCACTTTGGCTGTTTCACT 224  
QY 121 GCAGGCTTCTTAAACAGAACCACTGGGTGAATGTAATGAATTTGAAAAAATT 180  
|||||  
DB 225 GCAGGCTTCTTAAACAGAACCACTGGGTGAATGTAATGAATTTGAAAAAATT 284  
QY 181 GAAGATCTTATTCATCTATGATGCTACTTATTAATAGGAAAGTATGTTTCACT 240  
|||||  
DB 285 GAAGATCTTATTCATCTATGATGCTACTTATTAATAGGAAAGTATGTTTCACT 344  
QY 241 CCCAGTTGCAAAAGTAAACAGCAATGAAGTCTTCTTGGAGTTTCAAGTTATTTCACTT 300  
|||||  
DB 345 CCCAGTTGCAAAAGTAAACAGCAATGAAGTCTTCTTGGAGTTTCAAGTTATTTCACTT 404  
QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAAATTCGATCATCTGCAAAACAC 360  
|||||  
DB 405 GAGTCCGGAGATGCAAGTATTCATGATACAGTAAATTCGATCATCTGCAAAACAC 464  
QY 361 AGTTGTCTTCTAATGGAGATGTAACAGAAATCTGGATGCAA 401  
|||||  
DB 465 AGTTGTCTTCTAATGGAGATGTAACAGAAATCTGGATGCAA 505

## RESULT

4 Bg184658 800 bp mRNA linear EST 21-APR-2001

LOCUS Bg184658 R373720 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

DEFINITION Bg184658

ACCESSION Bg184658.1 GI:13706473

KEYWORDS EST.

ORGANISM human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

## AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 800)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
Cain, S., Leventhal, C., Thornton, M., Ramchandran, R., Whittington, J.,  
Lerner, B., Costanzo, D., McEligott, K., Boozer, S., Mays, R., Smith,  
E., Veloso, N., Klika, A., Hess, J., Colthron, K., Lo, K., Offenbacher,  
J., Danzig, J., and Ducar, M.

## TITLE

Creation of genome-wide protein expression libraries using random

## JOURNAL

Nat. Biotechnol. 19 (5), 440-445 (2001)

## MEDLINE

21227151

## COMMENT

Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave. Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@atersys.com  
High quality sequence stop: 444.

## FEATURES

## SOURCE

1. 800  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Athersys RAGE Library"  
/cell\_line="H1080"  
/note="See 'Creation of Genome-Wide Protein Expression Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
cell type indicated is H1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in H1080 under normal circumstances."

BASE COUNT  
ORIGIN

235 a 151 c 165 g 247 t

Query Match 71.3%; Score 348.8; DB 10; Length 800;  
Best Local Similarity 90.4%; Pred. No. 1.2e-71;  
Matches 441; Conservative 0; Mismatches 37; Indels 10; Gaps 6;

QY 1 ATGGAATTCGAAACACATTTGAGAAGTATTCATCCAGTGCCTACTTGTCTTACTT 60  
|||||  
DB 265 ATGGAATTCGAAACACATTTGAGAAGTATTCATCCAGTGCCTACTTGTCTTACTT 324  
QY 61 CTAAACAGTATTTCTTAACTGAAGTGGCATTCATCTTCACTTTGGCTGTTTCACT 120  
|||||  
DB 325 CTAAACAGTATTTCTTAACTGAAGTGGCATTCATCTTCACTTTGGCTGTTTCACT 384  
QY 121 GCAGGCTTCTTAAACAGAACCACTGGGTGAATGTAATGAATTTGAAAAAATT 180  
|||||  
DB 385 GCAGGCTTCTTAAACAGAACCACTGGGTGAATGTAATGAATTTGAAAAAATT 444  
QY 181 GAAGATCTTATTCATCTATGATGCTACTTATTAATAGGAAAGTATGTTTCACT 240  
|||||  
DB 445 GAAGATCTTATTCATCTATGATGCTACTTATTAATAGGAAAGTATGTTTCACT 504  
QY 241 CCCAGTTGCAAAAGTAAACAGCAATGAAGTCTTCTTGGAGTTTCAAGTTATTTCACTT 300  
|||||  
DB 505 CCCAGTTGCAAAAGTAAACAGCAATGAAGTCTTCTTGGAGTTTCAAGTTATTTCACTT 564  
QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAAATTCGATCATCTGCAAAACAC 360  
|||||  
DB 565 GAGTCCGGAGATGCAAGTATTCATGATACAGTAAATTCGATCATCTGCAAAACAC 622  
QY 361 AGTTGTCTTCTAATGGAGATGTAACAGAAATCTGGATGCAAAGTGAAGAACTGGAG 420  
|||||  
DB 623 A-TTTGGCTTCTAATGGAGTGT--ACAAATCTGGTGAAGATGAAGAACTGGAG 678  
QY 421 GAAAAAATTAATGAATTTTGGAGAGTTTGTACATATTTGCCAATGTTCATCAAC 480  
|||||  
DB 679 G--AAAAATTTAAGAAATTTTGAAGATTTTGGCTATTGG--CCAATGTTCTCAAC 734  
QY 481 ACTCTTG 488  
|||||  
DB 735 ACTTTTG 742



OY 474 CATCAACACTTCTTGA 489  
|||||  
Db 299 CATCAACACTTCTTGA 314

RESULT 7  
BI758686 872 bp mRNA linear EST 25-SEP-2001  
LOCUS 603024240F1 NIH\_MGC\_114 Homo sapiens CDNA clone IMAGE:5194977 5',  
DEFINITION mRNA sequence.  
ACCESSION BI758686  
VERSION BI758686.1 GI:15750264  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 872)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Plate: LLAM11487 row: 0 column: 10  
High quality sequence start: 24  
High quality sequence stop: 859.  
Location/Qualifiers

## FEATURES

source

1..872  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:5194977"  
/clone\_lib="NIH\_MGC\_114"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6  
male brains, age range 23-27 yo. Library is Oligo-dT  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.5 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 019. Note:  
this is a NIH\_MGC Library."  
BASE COUNT 200 a 222 c 227 g 223 t  
ORIGIN

Query Match 49.9%; Score 244; DB 10; Length 872;  
Best Local Similarity 98.9%; Pred. No. 4.1e-47;  
Matches 277; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

OY 1 ATGAGATTTCGAACACATTTGAGAAGATTTCCATCCAGTGTACTGTCTTACTT 60  
|||||  
Db 592 ATGAGATTTCGAACACATTTGAGAAGATTTCCATCCAGTGTACTGTCTTACTT 651  
OY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTATTTGGGCTGTTCACT 120  
|||||  
Db 652 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTATTTGGGCTGTTCACT 711  
OY 121 GCAGGCTTCCTAAACAGACAGCACTGGGTAAGTATAGTATTTGA-AAAAAT 179  
|||||  
Db 712 GCAGGCTTCCTAAACAGACAGCACTGGGTAAGTATAGTATTTGA-AAAAAT 771  
OY 180 TGAAGATCTTATTCATCTATGATATGATGCTACTTATATAGGAAGTATGTTCA 239  
|||||  
Db 772 TGAAGATCTTATTCATCTATGATATGATGCTACTTATATAGGAAGTATGTTCA 831

OY 240 -CCCCAGTTGCAAGTAACA-GCAATGAGTGCCTTCT 277  
|||||  
Db 832 CCCCCAGTTGCAAGTAACAAGTATGAGTGCCTTCT 871

RESULT 8  
BI685688 826 bp mRNA linear EST 18-SEP-2001  
LOCUS 603309529F1 NCI\_CGAP\_Mam6 Mus musculus CDNA clone IMAGE:5345382 5',  
DEFINITION mRNA sequence.  
ACCESSION BI685688  
VERSION BI685688.1 GI:15648316  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 826)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Jeffrey Green M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov

Plate: LLAM11877 row: 0 column: 07  
High quality sequence stop: 826.  
Location/Qualifiers

## FEATURES

source

1..826  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone\_lib="IMAGE:5345382"  
/clone\_lib="NCI\_CGAP\_Mam6"  
/sex="female, virgin"  
/tissue\_type="infiltrating ductal carcinoma"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Jeffrey Green, M.D., NIH"  
BASE COUNT 212 a 218 c 174 g 222 t  
ORIGIN

Query Match 43.1%; Score 210.6; DB 10; Length 826;  
Best Local Similarity 79.4%; Pred. No. 2.7e-39;  
Matches 274; Conservative 0; Mismatches 69; Indels 2; Gaps 2;

OY 1 ATGAGATTTCGAACACATTTGAGAAGATTTCCATCCAGTGTACTGTCTTACTT 60  
|||||  
Db 481 ATGAGATTTCGAACACATTTGAGAAGATTTCCATCCAGTGTACTGTCTTACTT 540  
OY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTATTTGGGCTGTTCACT 120  
|||||  
Db 541 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTATTTGGGCTGTTCACT 599  
OY 121 GCAGGCTTCCTAAACAGACAGCACTGGGTAAGTATAGTATTTGA-AAAAAT 180  
|||||  
Db 600 GTAGGCTTCCTAAACAGACAGCACTGGGTAAGTATAGTATTTGA-AAAAAT 659  
OY 181 GAAGATCTTATTCATCTATGATATGATGCTACTTATATAGGAAGTATGTTCA 240  
|||||  
Db 660 GAAGATCTTATTCATCTATGATATGATGCTACTTATATAGGAAGTATGTTCA 718  
OY 241 CCCAGTTGCAAGTAACAAGTATGAGTGCCTTCTTGGAGTTCAAGTATTTTCACTT 300  
|||||

Db 719 CCGAGTTCGAAGATTACTGCAATGACACTGTTTCCTCGAATTCGGCGTTATTATTACAT 778  
 Oy 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAAATTCGATC 345  
 Db 779 GAGTACAGTAACTGATGCTTAAATGAAACAGTAAACAGTGCCTC 823

RESULT 9  
 BF095213 309 bp mRNA linear EST 19-OCT-2000  
 LOCUS IL2-UT0071-050900-144-B03 UT0071 Homo sapiens cDNA, mRNA sequence.  
 DEFINITION BF095213  
 VERSION BF095213.1 GI:10900923  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 309)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
 Brunslein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 JOURNAL MEDLINE 20202663  
 COMMENT Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?rl=et2-IL2-UT0071-050  
 900-144-B03&t3=2000-09-05&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence stop: 309.  
 Location/Qualifiers  
 1..309  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_11b="UT0071"  
 /dev\_stage="Adult"  
 /note="Organ: uterus; tumor; Vector: puc18; Site\_1: Sma1;  
 Site\_2: Sma1; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 Profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 BASE COUNT 110 a 48 c 55 g 96 t  
 ORIGIN

Query Match 36.0%; Score 176.2; DB 10; Length 309;  
 Best Local Similarity 98.3%; Pred. No. 2.9e-31;  
 Matches 178; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 309 AGATCAAGTATTCATGATACGTAGAAATCTGATCATCCAGCAACAGATTGTC 368  
 Db 1 AGATCAAGTATTCATGATACGTAGAAATCTGATCATCCAGCAACAGATTGTC 60  
 Oy 369 TTCATATGGAGTGAACAGATCGATGCAAGAAATGAGGAAGTGGAGAAAAA 428  
 Db 61 TTCATATGGAGTGAACAGATCGATGCAAGAAATGAGGAAGTGGAGAAAAA 120  
 Oy 429 TATTAAGAAATTTTGCAGAGTTTGTACATATGTGCCAAATGTTTCATCAACACTTCTTG 488

Db 121 TATTAAGAAATTTTGCAGAGATTGTTGATCATATTGCCAAGTTCATCAACACTTCTTG 180  
 Oy 489 A 489  
 Db 181 A 181

RESULT 10  
 N76741 471 bp mRNA linear EST 02-APR-1996  
 LOCUS yz82g12.i1 Soares\_multiple\_sclerosis\_2NBHMSF Homo sapiens cDNA  
 DEFINITION clone IMAGE:289606 5' similar to SW:IL15\_HUMAN P40933  
 INTERLEUKIN-15 PRECURSOR ;, mRNA sequence.  
 N76741  
 VERSION N76741.1 GI:1239319  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 471)  
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman  
 M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,  
 Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treviski,E., Waterston  
 R., Williamson,A., Wohlmann,P. and Wilson,R.  
 The Mashu-Merck EST Project  
 Unpublished (1995)  
 JOURNAL MEDLINE 19950000  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: reverse ET  
 High quality sequence stop: 296.  
 Location/Qualifiers  
 1..471  
 /organism="Homo sapiens"  
 /db\_xref="GDB:3905446"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:289606"  
 /clone\_11b="Soares\_multiple\_sclerosis\_2NBHMSF"  
 /sex="male"  
 /tissue-type="multiple sclerosis lesions"  
 /dev\_stage="Age 46"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Vector: pRT3D (Pharmacia) with a modified  
 polylinker V-type; phagemid; Site\_1: Not I; Site\_2: Eco RI  
 primer 15',  
 TGTTCACATCTGAAGTGGAGCGGCCCATTTTCTTTTCTTTT 3',  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pRT3D vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis  
 lesions from one patient was kindly provided by Dr. Kevin  
 G. Becker (NINDS/NIH)."  
 BASE COUNT 161 a 68 c 83 g 154 t 5 others  
 ORIGIN

Query Match 35.6%; Score 174; DB 10; Length 471;  
 Best Local Similarity 97.4%; Pred. No. 9.8e-31;  
 Matches 185; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Db 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCCAGCAAC 360  
 Db 4 GAGTCCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCCAGCAAC 63

QY 361 AGTTGCTCTTAATGGAGATGTAACAGATCTGGATGCAAGAATGAGGAATCTGGAG 420  
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 Db 64 AGTTGCTCTTAATGGAGATGTAACAGATCTGGATGCAAGAATGAGGAATCTGGAG 123  
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 QY 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGCCAATGTCAT-CAA 479  
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 Db 124 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGCCAATGTCATNTNCAA 183  
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 QY 480 CACTTCTTGA 489  
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 Db 184 CACTTCTTGA 193  
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RESULT 11  
 A1596704  
 LOCUS 690 bp mRNA linear EST 21-APR-1999  
 DEFINITION V38h11.y1 Soares\_mammary\_gland\_NbMNG Mus musculus cDNA clone  
 IMAGE:948933 5' similar to gb:U14332 Mus musculus interleukin 15  
 (MOUSE); mRNA sequence.  
 A1596704  
 ACCESSION A1596704.1 GI:4605752  
 VERSION EST.  
 KEYWORDS house mouse.  
 SOURCE Mus musculus.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:345789  
 This read is a RESSEQUENCE of a previously sequenced mouse clone  
 This read has been verified (found to hit its original self in the  
 correct orientation)  
 Seq primer: -40RP from G1bco  
 High quality sequence stop: 466.  
 Location/Qualifiers  
 1. 690  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:948933"  
 /clone\_lib="Soares\_mammary\_gland\_NbMNG"  
 /sex="male"  
 /tissue\_type="mammary gland"  
 /dev\_stage="4 weeks"  
 /lab\_host="DH10B"  
 /note="Organ: mammary gland; Vector: p773D-Pac (Pharmacia  
 ) with a modified polylinker; Site\_1: Not I; Site\_2: Eco  
 RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
 primer [5'  
 TGTACCAATCTGAAGTGGAGCGCGCGCAATGCTTTTCTTTTCTTTTCTTTTCTTTT  
 T 3'] double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified p773 vector.  
 RNA provided by Dr. Minoru Ko, Wayne State Univ. Library  
 constructed and normalized by Bento Soares and M. Fatima  
 Bonaldo."

BASE COUNT 178 a 177 c 158 g 170 t 7 others  
 ORIGIN

Query Match 34.1%; Score 166.6; DB 9; Length 690;  
 Best Local Similarity 81.5%; Pred. No. 5.4e-29;  
 Matches 190; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACATTGAGAGATTTCATCCATCCAGTGTACTTGTGTACTTT 60

Db 450 ATGAAATTTGAAACCTATATATGAGAAATACATCCATCTGCTCTCTGTTCTT 509  
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 QY 61 CTAACAGTCATTTTCTTACTGAAGCTGCATTCATGCTTCATTTTGGCTGTTTCACT 120  
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 Db 510 CTAACAGTCATTTTCTTACTGAAGCTGCATTCATGCTTCATTTTGGCTGTTTCACT 569  
 |||||  
 QY 121 GCAGGCTCTCTTAACAGAGCCAACTGGGTGAATGATTAATAGTATTTGAAAAAATT 180  
 |||||  
 Db 570 GTAGCTCTCCCTAAACAGAGCCAACTGGGTGAATGATTAATAGTATTTGAAAAAATT 629  
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 QY 181 GAAGATCTTATTCATATGATGATGCTCTTATATAGCAAGTGA 233  
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 Db 630 GAAGATCTTATTCATATGATGATGCTCTTATATAGCAAGTGA 682  
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RESULT 12  
 N49734/c  
 LOCUS 474 bp mRNA linear EST 14-FEB-1996  
 DEFINITION y206b12.s1 Soares\_multiple\_sclerosis\_2NBHNSP Homo sapiens cDNA  
 clone IMAGE:282239 3' similar to SW:1115\_HUMAN P40933  
 INTERLEUKIN-15 PRECURSOR; mRNA sequence.  
 N49734  
 ACCESSION N49734.1 GI:1190900  
 VERSION EST.  
 KEYWORDS human.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 474)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman  
 Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston  
 R., Williamson, A., Wohlmann, P. and Wilson, R.  
 The WashU-Merck EST Project  
 Unpublished (1995)  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: m13 -40 forward  
 High quality sequence stop: 263.  
 Location/Qualifiers  
 1. 474  
 /organism="Homo sapiens"  
 /db\_xref="GDB:3900767"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:282239"  
 /clone\_lib="Soares\_multiple\_sclerosis\_2NBHNSP"  
 /sex="male"  
 /tissue\_type="multiple sclerosis lesions"  
 /dev\_stage="Age 46"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /note="Vector: p773D (Pharmacia) with a modified  
 polylinker V-type; phagemid; Site\_1: Not I; Site\_2: Eco RI  
 ; 1st strand cDNA was primed with a Not I - oligo(dT)  
 primer [5'  
 TGTACCAATCTGAAGTGGAGCGCGCGCAATGCTTTTCTTTTCTTTTCTTTTCTTTT  
 T 3'] double-stranded cDNA was size selected, ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified p773 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis  
 lesions from one patient was kindly provided by Dr. Kevin  
 G. Becker (MINDS/NIH)."

BASE COUNT 160 a 81 c 67 g 161 t 5 others  
 ORIGIN







---

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 01:32:22 ; Search time 2151.24 Seconds  
(without alignments)  
4756.827 Million cell updates/sec

Title: US-09-724-841-4  
Perfect score: 489  
Sequence: 1 ATGAGATTTCGAAACCA.....TGTTCATCAACACTTCTGA 489

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: gb\_da:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vi:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	489	100.0	489	6	AR004267	Sequence 1 from patent US 5747024.	DNA	linear	PAT 04-DEC-1998
2	489	100.0	489	6	AR024348				
3	489	100.0	489	6	AR070282				
4	489	100.0	489	6	AR085741				
5	489	100.0	489	6	AR122045				
6	489	100.0	489	6	AR122867				
7	489	100.0	489	6	AR125104				
8	489	100.0	489	6	AX006785				
9	489	100.0	489	6	125782				
10	489	100.0	489	6	128850				
11	489	100.0	489	6	179220				
12	489	100.0	1275	9	CAU03099				
13	484.2	99.0	492	9	AB000555				
14	484.2	99.0	559	9	MMU19843				
15	465	95.1	489	6	AR004268				
16	465	95.1	489	6	AR024349				
17	465	95.1	489	6	AR070281				
18	465	95.1	489	6	AR085740				
19	465	95.1	489	6	AR122046				
20	465	95.1	489	6	AR122868				
21	465	95.1	489	6	AR125105				
22	465	95.1	489	6	AX006786				
23	465	95.1	489	6	AX320244				
24	465	95.1	489	6	125783				
25	465	95.1	489	6	128849				
26	465	95.1	489	6	162692				
27	465	95.1	489	6	179219				
28	465	95.1	1202	6	AR103280				
29	465	95.1	1202	6	AX024715				
30	465	95.1	1202	6	AX301227				
31	465	95.1	1202	6	HS014407				
32	463.4	94.8	489	6	AR094649				
33	463.4	94.8	489	6	BD008811				
34	458.6	93.8	489	6	AX320242				
35	457	93.5	489	6	AR094650				
36	457	93.5	489	6	BD008812				
37	430.6	88.1	459	6	HS1115MR				
38	385	78.7	489	4	BTU42433				
39	381.8	78.1	489	4	SSU58142				
40	375.4	76.8	489	4	AF149700				
41	372.2	76.1	489	4	AF108148				
42	359.2	73.5	643	9	HS1115MR1				
43	359.2	73.5	643	9	HS1115MR2				
44	357.6	73.1	1248	6	AR087004				
45	357.6	73.1	1248	9	AF031167				

## ALIGNMENTS

RESULT	1	489 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR004267				
DEFINITION	Sequence 1 from patent US 5747024.				
ACCESSION	AR004267				
VERSION	AR004267.1	GI:3965146			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 489)				
AUTHORS	Grabstein,K.H. and Widmer,M.B.				
TITLE	Vaccine adjuvant comprising Interleukin-15				
JOURNAL	Patent: US 5747024-A 1 05-MAY-1998;				
FEATURES	Location/Qualifiers				
source	1..489				
BASE COUNT	162 a 81 c 92 g 154 t				
ORIGIN					
Query Match	100.0%	Score 489;	DB 6;	Length 489;	
Best Local Similarity	100.0%;	Pred. No. 5,4e-91;			

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTTGGAACACATTTGAGAGATTTCCATCCAGTGTACCTGTGTTACTT 60  
|  
Db 1 ATGGAATTTGGAACACATTTGAGAGATTTCCATCCAGTGTACCTGTGTTACTT 60  
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QY 61 CTAAGAGATCTTTCTAAGTGAAGTGCATTCATGCTCTTCAATTTGGGCTGTTCAGT 120  
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Db 61 CTAAGAGATCTTTCTAAGTGAAGTGCATTCATGCTCTTCAATTTGGGCTGTTCAGT 120  
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QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGAATTTGAAAAAATT 180  
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Db 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGAATTTGAAAAAATT 180  
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QY 181 GAAGATCTTTATCAATCTATGATATTTGATGCTACTTTATACAAAGTGTTCAC 240  
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Db 181 GAAGATCTTTATCAATCTATGATATTTGATGCTACTTTATACAAAGTGTTCAC 240  
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QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTTGAGATTGCAAGTTATTTCCAT 300  
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Db 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTTGAGATTGCAAGTTATTTCCAT 300  
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QY 301 GAGTCCGGAGATACAGATATTTGATGATGATGAGAAATCTTATCTCTAGCAACAC 360  
|  
Db 301 GAGTCCGGAGATACAGATATTTGATGATGATGAGAAATCTTATCTCTAGCAACAC 360  
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QY 361 ATCTGTCTTCTAATGGAATATACAGATCTGATGCAAGAAATGTGAGAACTAGAG 420  
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Db 361 ATCTGTCTTCTAATGGAATATACAGATCTGATGCAAGAAATGTGAGAACTAGAG 420  
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QY 421 GAAAAAATATTAAAGAAATTTTGGAGATTTTGTACATATTTGCCAAATGTTTCATCAAC 480  
|  
Db 421 GAAAAAATATTAAAGAAATTTTGGAGATTTTGTACATATTTGCCAAATGTTTCATCAAC 480  
|  
QY 481 ACTTCTTGA 489  
|  
Db 481 ACTTCTTGA 489  
|

RESULT 2

AR024348 489 bp DNA linear PAT 05-DEC-1998

LOCUS AR024348 489 bp DNA linear PAT 05-DEC-1998

DEFINITION Sequence 1 from patent US 5795966.

ACCESSION AR024348

VERSION AR024348.1 GI:3977642

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 489)

AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.

TITLE Antagonists of interleukin-15

JOURNAL Patent: US 5795966-A 1 18-AUG-1998;

FEATURES

source 1. 489

BASE COUNT 162 a 81 c 92 g 154 t

ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 5.4e-91;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTTGGAACACATTTGAGAGATTTCCATCCAGTGTACCTGTGTTACTT 60  
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Db 1 ATGGAATTTGGAACACATTTGAGAGATTTCCATCCAGTGTACCTGTGTTACTT 60  
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QY 61 CTAAGAGATCTTTCTAAGTGAAGTGCATTCATGCTCTTCAATTTGGGCTGTTCAGT 120  
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Db 61 CTAAGAGATCTTTCTAAGTGAAGTGCATTCATGCTCTTCAATTTGGGCTGTTCAGT 120  
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QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGAATTTGAAAAAATT 180  
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Db 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGAATTTGAAAAAATT 180  
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QY 181 GAAGATCTTTATCAATCTATGATATTTGATGCTACTTTATACAAAGTGTTCAC 240  
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QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTTGAGATTGCAAGTTATTTCCAT 300  
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Db 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTTGAGATTGCAAGTTATTTCCAT 300  
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Db 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGAATTTGAAAAAATT 180  
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QY 181 GAAGATCTTTATCAATCTATGATATTTGATGCTACTTTATACAAAGTGTTCAC 240  
|  
Db 181 GAAGATCTTTATCAATCTATGATATTTGATGCTACTTTATACAAAGTGTTCAC 240  
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QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTTGAGATTGCAAGTTATTTCCAT 300  
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Db 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTTGAGATTGCAAGTTATTTCCAT 300  
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Db 301 GAGTCCGGAGATACAGATATTTGATGATGATGAGAAATCTTATCTCTAGCAACAC 360  
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QY 361 ATCTGTCTTCTAATGGAATATACAGATCTGATGCAAGAAATGTGAGAACTAGAG 420  
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Db 361 ATCTGTCTTCTAATGGAATATACAGATCTGATGCAAGAAATGTGAGAACTAGAG 420  
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QY 421 GAAAAAATATTAAAGAAATTTTGGAGATTTTGTACATATTTGCCAAATGTTTCATCAAC 480  
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Db 421 GAAAAAATATTAAAGAAATTTTGGAGATTTTGTACATATTTGCCAAATGTTTCATCAAC 480  
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QY 481 ACTTCTTGA 489  
|  
Db 481 ACTTCTTGA 489  
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RESULT 3

AR070282 489 bp DNA linear PAT 18-FEB-2000

LOCUS AR070282 489 bp DNA linear PAT 18-FEB-2000

DEFINITION Sequence 4 from patent US 5892001.

ACCESSION AR070282

VERSION AR070282.1 GI:7221170

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 489)

AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.

TITLE Epstein-Barr virus-derived T-cell factor antibodies

JOURNAL Patent: US 5892001-A 4 06-APR-1999;

FEATURES

source 1. 489

BASE COUNT 162 a 81 c 92 g 154 t

ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 5.4e-91;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTTGGAACACATTTGAGAGATTTCCATCCAGTGTACCTGTGTTACTT 60  
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Db 1 ATGGAATTTGGAACACATTTGAGAGATTTCCATCCAGTGTACCTGTGTTACTT 60  
|  
QY 61 CTAAGAGATCTTTCTAAGTGAAGTGCATTCATGCTCTTCAATTTGGGCTGTTCAGT 120  
|  
Db 61 CTAAGAGATCTTTCTAAGTGAAGTGCATTCATGCTCTTCAATTTGGGCTGTTCAGT 120  
|  
QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGAATTTGAAAAAATT 180  
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Db 121 GCAGGGCTCCCTAAACAGAACCACTGGGTAAATGTAATGAATTTGAAAAAATT 180  
|  
QY 181 GAAGATCTTTATCAATCTATGATATTTGATGCTACTTTATACAAAGTGTTCAC 240  
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Db 181 GAAGATCTTTATCAATCTATGATATTTGATGCTACTTTATACAAAGTGTTCAC 240  
|  
QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTTGAGATTGCAAGTTATTTCCAT 300  
|  
Db 241 CCCAGTTGCAAGTAAACAGCAATGAAGTCTTCTTGAGATTGCAAGTTATTTCCAT 300  
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QY 301 GAGTCGGAGATACAGATATTCATGATACAGTACAGAAATCTTATCATCTCTAGCAAAACAC 360  
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Db 301 GAGTCGGAGATACAGATATTCATGATACAGTACAGAAATCTTATCATCTCTAGCAAAACAC 360  
QY 361 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420  
|||||  
Db 361 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420  
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGTCACAAATGTTTCATCAAC 480  
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Db 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGTCACAAATGTTTCATCAAC 480  
QY 481 ACTTCTTGA 489  
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Db 481 ACTTCTTGA 489  
RESULT 4  
AR085741 AR085741 489 bp DNA linear PAT 07-SEP-2000  
LOCUS AR085741 4 from patent US 5985262.  
DEFINITION Sequence  
ACCESSION AR085741  
VERSION AR085741.1 GI:10012507  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Method of treatment with epithelium derived T-cell factor  
JOURNAL Patent: US 5985262-A 4 16-NOV-1999;  
FEATURES  
source 1..489  
/organism="unknown"  
BASE COUNT 162 a 81 c 92 g 154 t  
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 5.4e-91;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACACATTTGAGAGATATTCATCCAGTGCCTGCTGTTTACTT 60  
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Db 1 ATGAGATTTTGAACACATTTGAGAGATATTCATCCAGTGCCTGCTGTTTACTT 60  
QY 61 CTAAGAGTATTTTCTAATCTAGTGAAGTGGCATTCATGCTTTCATTTTGGCTGTTTCACT 120  
|||||  
Db 61 CTAAGAGTATTTTCTAATCTAGTGAAGTGGCATTCATGCTTTCATTTTGGCTGTTTCACT 120  
QY 121 GCAGGCTCCCTAAACAGAGCCACTGGGTGAATGTATTAAGTGAATTTGAAAAAATT 180  
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Db 121 GCAGGCTCCCTAAACAGAGCCACTGGGTGAATGTATTAAGTGAATTTGAAAAAATT 180  
QY 181 GAAGATCTTATTCATATGATATGATGCTTCTTATATACAGAAAGTATGTTTCAAC 240  
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Db 181 GAAGATCTTATTCATATGATATGATGCTTCTTATATACAGAAAGTATGTTTCAAC 240  
QY 241 CCCAGTTGCAAGTATACAGCAATGAAGTCTTCTGTTGCAAGTTTATTTTCACT 300  
|||||  
Db 241 CCCAGTTGCAAGTATACAGCAATGAAGTCTTCTGTTGCAAGTTTATTTTCACT 300  
QY 301 GAGTCGGAGATACAGATATTCATGATACAGTAAATCTTATCATCTCTAGCAAAACAC 360  
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Db 301 GAGTCGGAGATACAGATATTCATGATACAGTAAATCTTATCATCTCTAGCAAAACAC 360  
QY 361 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420  
|||||  
Db 361 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420  
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGTCACAAATGTTTCATCAAC 480  
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Db 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGTCACAAATGTTTCATCAAC 480

QY 481 ACTTCTTGA 489  
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Db 481 ACTTCTTGA 489  
RESULT 5  
AR122045 AR122045 489 bp DNA linear PAT 16-MAY-2001  
LOCUS AR122045 1 from patent US 6165466.  
DEFINITION Sequence  
ACCESSION AR122045  
VERSION AR122045.1 GI:14106362  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 489)  
AUTHORS Grabstein,K.H., Pettil,D.K. and Paxton,R.J.  
TITLE Antagonists of interleukin-15  
JOURNAL Patent: US 6165466-A 1 26-DEC-2000;  
FEATURES  
source 1..489  
/organism="unknown"  
BASE COUNT 162 a 81 c 92 g 154 t  
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
Best Local Similarity 100.0%; Pred. No. 5.4e-91;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACACATTTGAGAGATATTCATCCAGTGCCTGCTGTTTACTT 60  
|||||  
Db 1 ATGAGATTTTGAACACATTTGAGAGATATTCATCCAGTGCCTGCTGTTTACTT 60  
QY 61 CTAAGAGTATTTTCTAATCTAGTGAAGTGGCATTCATGCTTTCATTTTGGCTGTTTCACT 120  
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Db 61 CTAAGAGTATTTTCTAATCTAGTGAAGTGGCATTCATGCTTTCATTTTGGCTGTTTCACT 120  
QY 121 GCAGGCTCCCTAAACAGAGCCACTGGGTGAATGTATTAAGTGAATTTGAAAAAATT 180  
|||||  
Db 121 GCAGGCTCCCTAAACAGAGCCACTGGGTGAATGTATTAAGTGAATTTGAAAAAATT 180  
QY 181 GAAGATCTTATTCATATGATATGATGCTTCTTATATACAGAAAGTATGTTTCAAC 240  
|||||  
Db 181 GAAGATCTTATTCATATGATATGATGCTTCTTATATACAGAAAGTATGTTTCAAC 240  
QY 241 CCCAGTTGCAAGTATACAGCAATGAAGTCTTCTGTTGCAAGTTTATTTTCACT 300  
|||||  
Db 241 CCCAGTTGCAAGTATACAGCAATGAAGTCTTCTGTTGCAAGTTTATTTTCACT 300  
QY 301 GAGTCGGAGATACAGATATTCATGATACAGTAAATCTTATCATCTCTAGCAAAACAC 360  
|||||  
Db 301 GAGTCGGAGATACAGATATTCATGATACAGTAAATCTTATCATCTCTAGCAAAACAC 360  
QY 361 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420  
|||||  
Db 361 ATCTGTCTCTTAATGGAATATATACAGATCTGATCAAAAGATGAGAACTAGAG 420  
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGTCACAAATGTTTCATCAAC 480  
|||||  
Db 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGTCACAAATGTTTCATCAAC 480

RESULT 6  
AR122867 AR122867 489 bp DNA linear PAT 16-MAY-2001  
LOCUS AR122867  
DEFINITION Sequence 1 from patent US 6168783.  
ACCESSION AR122867

VERSION AR122867.1 GI:14107833  
 KEYWORDS UNKNOWN.  
 SOURCE UNKNOWN.  
 ORGANISM UNKNOWN.

REFERENCE 1 (bases 1 to 489)  
 AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.  
 TITLE Antagonists of Interleukin-15  
 JOURNAL Patent: US 6168783-A 1 02-JAN-2001;  
 FEATURES Location/Qualifiers  
 source 1..489

BASE COUNT 162 a 81 c 92 g 154 t  
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-91;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACATTTGAGAGATTTCATCCAGTGCCTGCTTACTT 60  
 DB 1 ATGAGATTTCGAACACATTTGAGAGATTTCATCCAGTGCCTGCTTACTT 60  
 QY 61 CTAAAGATCTATTCTAATCTAAGCTGSCATTCATCTTCATTTTGGCTGTTCACT 120  
 DB 61 CTAAAGATCTATTCTAATCTAAGCTGSCATTCATCTTCATTTTGGCTGTTCACT 120  
 QY 121 GCAGGGCTCCCTAAACAGACCAAGCTGGTGAATGTAAAGTATTGAAAAAATT 180  
 DB 121 GCAGGGCTCCCTAAACAGACCAAGCTGGTGAATGTAAAGTATTGAAAAAATT 180  
 QY 181 GAAGATCTTATTCATCTATGATATTTGATCTACTTTATATACAGAAAGTATGTCAC 240  
 DB 181 GAAGATCTTATTCATCTATGATATTTGATCTACTTTATATACAGAAAGTATGTCAC 240  
 QY 241 CCCAGTTCGCAAGATTAAGCAATGAAGTCTTCTCTTGAGAGTTCAGAAATTTTCACT 300  
 DB 241 CCCAGTTCGCAAGATTAAGCAATGAAGTCTTCTCTTGAGAGTTCAGAAATTTTCACT 300  
 QY 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATGCTGCAACAAAC 360  
 DB 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATGCTGCAACAAAC 360  
 QY 361 ATCTTGCTTCTAATGGAATATTAACAGAAATCTGATGCAAAAGATGTGAGAACTAGAG 420  
 DB 361 ATCTTGCTTCTAATGGAATATTAACAGAAATCTGATGCAAAAGATGTGAGAACTAGAG 420  
 QY 421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTGTCCAAAATGTCATCAAC 480  
 DB 421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTGTCCAAAATGTCATCAAC 480  
 QY 481 ACTTCTTGA 489  
 DB 481 ACTTCTTGA 489

RESULT 7  
 LOCUS AR125104 489 bp DNA linear PAT 16-MAY-2001  
 DEFINITION Sequence 1 from patent US 6177079.  
 ACCESSION AR125104  
 VERSION AR125104.1 GI:14111166  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 489)  
 AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.  
 TITLE Antagonists of Interleukin-15  
 JOURNAL Patent: US 6177079-A 1 23-JAN-2001;  
 FEATURES Location/Qualifiers  
 source 1..489

BASE COUNT 162 a 81 c 92 g 154 t  
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-91;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACATTTGAGAGATTTCATCCAGTGCCTGCTTACTT 60  
 DB 1 ATGAGATTTCGAACACATTTGAGAGATTTCATCCAGTGCCTGCTTACTT 60  
 QY 61 CTAAAGATCTATTCTAATCTAAGCTGSCATTCATCTTCATTTTGGCTGTTCACT 120  
 DB 61 CTAAAGATCTATTCTAATCTAAGCTGSCATTCATCTTCATTTTGGCTGTTCACT 120  
 QY 121 GCAGGGCTCCCTAAACAGACCAAGCTGGTGAATGTAAAGTATTGAAAAAATT 180  
 DB 121 GCAGGGCTCCCTAAACAGACCAAGCTGGTGAATGTAAAGTATTGAAAAAATT 180  
 QY 181 GAAGATCTTATTCATCTATGATATTTGATCTACTTTATATACAGAAAGTATGTCAC 240  
 DB 181 GAAGATCTTATTCATCTATGATATTTGATCTACTTTATATACAGAAAGTATGTCAC 240  
 QY 241 CCCAGTTCGCAAGATTAAGCAATGAAGTCTTCTCTTGAGAGTTCAGAAATTTTCACT 300  
 DB 241 CCCAGTTCGCAAGATTAAGCAATGAAGTCTTCTCTTGAGAGTTCAGAAATTTTCACT 300  
 QY 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATGCTGCAACAAAC 360  
 DB 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATGCTGCAACAAAC 360  
 QY 361 ATCTTGCTTCTAATGGAATATTAACAGAAATCTGATGCAAAAGATGTGAGAACTAGAG 420  
 DB 361 ATCTTGCTTCTAATGGAATATTAACAGAAATCTGATGCAAAAGATGTGAGAACTAGAG 420  
 QY 421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTGTCCAAAATGTCATCAAC 480  
 DB 421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTGTCCAAAATGTCATCAAC 480  
 QY 481 ACTTCTTGA 489  
 DB 481 ACTTCTTGA 489

RESULT 8  
 LOCUS AX006785 489 bp DNA linear PAT 06-SEP-2000  
 DEFINITION Sequence 3 from Patent WO0002582.  
 ACCESSION AX006785  
 VERSION AX006785.1 GI:9994821  
 KEYWORDS  
 SOURCE unidentified.  
 ORGANISM unidentified.  
 REFERENCE 1 (bases 1 to 489)  
 AUTHORS Londel,M., Quarantino,S. and Maiuri,L.  
 TITLE Treatment of coliac disease with interleukin-15 antagonists  
 JOURNAL Patent: WO 0002582-A 3 20-JAN-2000;  
 LONDEI MARCO (GB); QUARANTINO SONIA (GB); MATHILDA AND TERENCE KENNEDY I (GB); MAIURI LUIGI (IT)  
 FEATURES Location/Qualifiers  
 source 1..489

BASE COUNT 162 a 81 c 92 g 154 t  
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-91;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAAATTTGAAACCCACATTTGGAGATTTTCCATCCAGCTGCTACTGGTTACTT	60
Db	1	ATGGAATTTTGAACCCACATTTGGAGATTTTCCATCCAGCTGCTACTGGTTACTT	60
QY	61	CTAAAGAGTCATTTTCTTAAGTCGAGCTGGCATTCATGTTCTCATTTTGGGCTGTTTCAGT	120
Db	61	CTAAAGAGTCATTTTCTTAAGTCGAGCTGGCATTCATGTTCTCATTTTGGGCTGTTTCAGT	120
QY	121	GCAGGGCTCCCTAAAGACGAAAGCCAACTGGGTGATGTATTAAGCATTTGAAAAAATT	180
Db	121	GCAGGGCTCCCTAAAGACGAAAGCCAACTGGGTGATGTATTAAGCATTTGAAAAAATT	180
QY	181	GAAGATCTTATTCATCATTCATCATTTATGCTACTTATATACAGAAAGTATGTTTAC	240
Db	181	GAAGATCTTATTCATCATTCATCATTTATGCTACTTATATACAGAAAGTATGTTTAC	240
QY	241	CCCACTTCCAGGTATACAGCAATGAAGCTTCTCTTGGAGTTGCAAGTATTTTCACAT	300
Db	241	CCCACTTCCAGGTATACAGCAATGAAGCTTCTCTTGGAGTTGCAAGTATTTTCACAT	300
QY	301	GAGTCGCGAGATACAGATATTCATCATTCACAGTAGAAAAATCTTATGATCCTGACCAAC	360
Db	301	GAGTCGCGAGATACAGATATTCATCATTCACAGTAGAAAAATCTTATGATCCTGACCAAC	360
QY	361	ATCTTGCTTTCTAATGGGAATATTAACACAATCTGGATGCCAAAGATGTGAGGACTAGAG	420
Db	361	ATCTTGCTTTCTAATGGGAATATTAACACAATCTGGATGCCAAAGATGTGAGGACTAGAG	420
QY	421	GAAGAAAAATATTAAGAAATTTTTCGAGAGTTTGTACATATTTGTCCAATGTTCTTCAAC	480
Db	421	GAAGAAAAATATTAAGAAATTTTTCGAGAGTTTGTACATATTTGTCCAATGTTCTTCAAC	480
QY	481	ACTTCTTGA 489	
Db	481	ACTTCTTGA 489	

[illegible]

Db	121	GCAGGGCTCCCTAAACAGAACCCCACTGGGATGTGTAATAAGGATTTGAAAAAANT	180
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Db	181	GAGATCTTATTCAACTCTATGCAATGATTTGATGCTACTTTATATACAGAAAGTATGTTCAAC	240
Oy	241	CCCACTTCGAGGTAAACGCAATGAAAGTCTTCTCTGGACTTCCAACTTATTTCCACAT	300
Db	241	CCCACTTCGAGGTAAACGCAATGAAAGTCTTCTCTGGAGTTCGAACTTATTTCCACAT	300
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Oy	361	ATCTTGTCCTCTTAATGGGAATATAACAGAAATCTGATGCAAGAAATGTGAGGAACTAGAG	420
Db	361	ATCTTGTCCTCTTAATGGGAATATAACAGAAATCTGATGCAAGAAATGTGAGGAACTAGAG	420
Oy	421	GAAAAAATATTTAAAGATTTTTGCAAGATTTGTACATATTTGTCGCAATGTTTCATCAAC	480
Db	421	GAAAAAATATTTAAAGATTTTTGCAAGATTTGTACATATTTGTCGCAATGTTTCATCAAC	480
Oy	481	ACTTCTTGA 489	
Db	481	ACTTCTTGA 489	

LOCUS	128850	128850	489 bp	DNA	linear	PAT 06-FEB-1997
DEFINITION	Sequence 4 from patent US 5574138.					
ACCESSION	128850					
VERSION	128850.1	GI:1819631				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 489)					
AUTHORS	Gradshteyn, K. H., Anderson, D. M., Eisenman, J. R., Fung, V. and Rauch, C.					
TITLE	Epithelium-derived T-cell factor					
JOURNAL	Patent: US 5574138-A 4 12-NOV-1996;					
FEATURES	Location/Qualifiers					
source	1..489					
BASE COUNT	162 a 81 c 92 g 154 t					
ORIGIN	/organism="unknown"					
Query Match	100.0%;	Score 489;	DB 6;	Length 489;		
Best Local Similarity	100.0%;	Pred. No. 5,4e-91;				
Matches	489; Conservative	0; Mismatches	0; Indels	0; Gaps	0;	
QY	1 ATGAGATTTTCCAAACCCACATTTTGAGAGATATTTCCATCCATCGCTACTGCTTACTT	60				
DB	1 ATGAGATTTTCCAAACCCACATTTTGAGAGATATTTCCATCCATCGCTACTGCTTACTT	60				
QY	61 CTTAAGAGTCATATTTCTACTAGACCTGGCATTCATATGTTCTCATTTTGGCGTGTTCAC	120				
DB	61 CTTAAGAGTCATATTTCTACTAGACCTGGCATTCATATGTTCTCATTTTGGCGTGTTCAC	120				
QY	121 GGAGGCGTCCCTTAAACAGAACCAACCTGGGTGATGTAAATAGCATTTTGAATAAAT	180				
DB	121 GGAGGCGTCCCTTAAACAGAACCAACCTGGGTGATGTAAATAGCATTTTGAATAAAT	180				
QY	181 GAGATCTTATTCATCTATGATATGTATGCTACTTTTATACAGAAAGTATGTTCC	240				
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QY	241 CCCAGTTGCAAGCTAACACACATGAAGTCTTCTTCTTGAGATTTGCAATATTTCACAT	300				
DB	241 CCCAGTTGCAAGCTAACACACATGAAGTCTTCTTCTTGAGATTTGCAATATTTCACAT	300				
QY	301 GAGTCCGGAGATACGATATTATCATATACGTAGAAAATCTTATCATCCTACCAACACAC	360				

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Qy 421 GAAAAAATATTAAGATTTTTCAGAGATTTTGTACATATTTGCCAAATGTTCAAC 480
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Qy 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 11
LOCUS I79220 489 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 4 from patent US 5707616.
ACCESSION I79220
VERSION I79220.1 GI:3207510
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein, K.H., Anderson, D.M., Eisenman, J.R., Fung, V. and Rauch, C.
TITLE Method for treating or preventing gastrointestinal disease with
epithelium-derived T-cell factor
JOURNAL Patent: US 5707616-A 4 13-JAN-1998;
FEATURES
source 1. 489
location/Qualifiers
BASE COUNT 162 a 81 c 92 g 154 t
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 5,4e-91;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCATCTTACCAAAACAC 360
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Qy 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 12
LOCUS CAU03099 1275 bp mRNA linear PRI 25-MAY-1994
DEFINITION Cercopithecus aethiops simian Interleukin 15 mRNA, complete cds.
ACCESSION U03099
VERSION U03099.1 GI:493521
KEYWORDS
SOURCE African green monkey.
ORGANISM Cercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
REFERENCE 1 (bases 1 to 1275)
AUTHORS Grabstein, K.H., Eisenman, J., Shanebeck, K., Rauch, C., Srinivasan, S.,
Johnson, L., Beers, C., Richardson, J., Schoenborn, M.A., Ahdieh, M.,
Fung, V., Anderson, M.R., Watson, J.D., Anderson, D.M. and Girdl, J.G.
TITLE Cloning of a T cell growth factor that interacts with the beta
chain of the interleukin-2 receptor
JOURNAL Science 264, 965-968 (1994)
MEDLINE 94233380
REFERENCE 2 (bases 1 to 1275)
AUTHORS Anderson, D.M.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1993) Dirk M. Anderson, Immunex Research and
Development Corp., 51 University St., Seattle, WA 98101, USA
FEATURES
source 1. 1275
location/Qualifiers
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484..972
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BASE COUNT 366 a 264 c 278 g 367 t
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Query Match 100.0%; Score 489; DB 9; Length 1275;
Best Local Similarity 100.0%; Pred. No. 4,5e-91;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 484 ATGAGATTTTGAACACACATTTGAGAGTATTTCCATCCAGTGTCTTACTT 543
Qy 61 CTAAGAGTCAATTTCTAATGCAAGCTGGCATTCATGTCCTTCAATTTGGGCTGTTCACT 120
Db 544 CTAAGAGTCAATTTCTAATGCAAGCTGGCATTCATGTCCTTCAATTTGGGCTGTTCACT 603
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anag

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TS"

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variation  
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BASE COUNT 179 a 93 c 105 g 182 t

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Best Local Similarity 99.4%; Pred. No. 5.1e-90;  
Matches 486; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAAATATTCATCCAGTGCCTACTGTTACTT 60  
DB 28 ATGAGAAATTCGAAACACATTTGAGAAATATTCATCCAGTGCCTACTGTTACTT 87  
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DB 88 CTAAAGAGTCATTTCTAATCTAAGTGCATTCATGCTTCATTTTGGCTGTTTCACT 147  
QY 121 GCAGGGCTCCCTAAACAGAACCACTGGTGATGTATTAAGTATTTGAAAAAATT 180  
DB 148 GCAGGGCTCCCTAAACAGAACCACTGGTGATGTATTAAGTATTTGAAAAAATT 207  
QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATACAGAAAGTATGTTTCA 240  
DB 208 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATACAGAAAGTATGTTTCA 267  
QY 241 CCCAGTTCGAGTAACAGCAATGAAGTCTTCTCTGGAGTGCAGATATTTTCACT 300  
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QY 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTATCATCTAGCAAAACAC 360  
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QY 481 ACTTCTTGA 489  
DB 508 ACTTCTTGA 516

RESULT 15  
LOCUS AR004268 489 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 4 from patent US 5747024.  
ACCESSION AR004268  
VERSION AR004268.1 GI:3965147  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 489)

AUTHORS Grabstein, K.H. and Widmer, M.B.  
TITLE Vaccine adjuvant comprising Interleukin-15  
JOURNAL Patent: US 5747024-A 4 05-May-1998.  
FEATURES Location/Qualifiers  
source 1..489  
BASE COUNT 159 a 79 c 95 g 156 t  
ORIGIN

Query Match 95.1%; Score 465; DB 6; Length 489;  
Best Local Similarity 96.9%; Pred. No. 4.7e-86;  
Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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QY 61 CTAAAGAGTCATTTCTAATCTAAGTGCATTCATGCTTCATTTTGGCTGTTTCACT 120  
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QY 121 GCAGGGCTCCCTAAACAGAACCACTGGTGATGTATTAAGTATTTGAAAAAATT 180  
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QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATACAGAAAGTATGTTTCA 240  
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DB 361 ATCTTGCTCTTAAATGGAAATTAACAGAAATCTGATGCAGAAAGTATGAGAACTAGAG 420  
QY 421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTTGCCAAATGTTTCACTCAAC 480  
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QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489

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Job time: 4951 sec





GenCore version 4.5  
2003 - 2000 CompuGen Ltd.

search, using sw model

JUNE 1971

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Gapop 10.0 , Gapext 1.0

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hills sacro-

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watch 08

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Maximum Match 45 summary

Listing first 45 summer

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09:14:02 2002
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Copyright (C) 1993 - 2000
etc search, using sw model
June 19, 2002, 00:56:15 ;

US-09-724-841-4
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hits satisfying chosen parameters
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11	/SIDSI/gcgdata/gen	489	17	P	14
12	/SIDSI/gcgdata/gen	489	17	P	14
13	/SIDSI/gcgdata/gen	489	17	P	14
14	/SIDSI/gcgdata/gen	489	17	P	14
15	/SIDSI/gcgdata/gen	489	17	P	14
16	/SIDSI/gcgdata/gen	489	17	P	14
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19	/SIDSI/gcgdata/gen	489	17	P	14
20	/SIDSI/gcgdata/gen	489	17	P	14
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22	/SIDSI/gcgdata/gen	489	17	P	14
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09:14:02 2002
GenCore version 1.0
Copyright (c) 1993 - 2000

eic search, using sw model

June 19, 2002, 00:56:15 ;

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IDENTITY NUC
Gapex 10.0 , Gapexl 1.0
1736436 seqs, 858457221
hits satisfying chosen Pa
length: 2000000000
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RESULT 3  
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 ID AAT49456 standard; cDNA; 489 BP.  
 AC AAT49456;  
 DT 11-MAR-1997 (first entry)  
 XX  
 DE Human epithelium derived T cell factor cDNA.  
 XX  
 KW hERT; human IMTLH bone marrow stromal cell line; T-cell; B-cell;  
 KW lymphocyte; proliferation; differentiation; gastrointestinal;  
 KW HIV infection; human immunodeficiency virus; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
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 FT /tag= a  
 FT mat-peptide 145..486  
 FT /tag= D  
 FT /product= hERT  
 XX  
 PN US5574138-A.  
 XX  
 PD 12-NOV-1996.  
 XX  
 PF 08-MAR-1993; 93US-0031399.  
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 PR 22-FEB-1995; 95US-0393305.  
 PR 08-MAR-1993; 93US-0031399.  
 PR 22-APR-1994; 94US-0233606.  
 XX  
 PA (IMMV) IMMUNEX CORP.  
 XX  
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
 PI Rauch C;  
 XX  
 DR WP1; 1996-517923/51.  
 DR P-PSDB; AAW09100 AND AAW09101.  
 XX  
 PT New epithelium derived T cell factor - induces proliferation of T

PT and B cells, stimulates destruction of tumour and virus-infected  
 PT cells and protects against toxicity, partic. for treating intestinal  
 PT disease and HIV infection  
 XX  
 PS Claim 1; Fig 2; 35pp; English.  
 XX  
 CC Human EMT (epithelium derived T cell factor) cDNA was isolated by  
 CC screening a IMTLH cell cDNA library with a simian EMT probe. The  
 CC IMTLH cell line was derived from a stable transformation of a human  
 CC bone marrow stromal cell culture with pSVNeo. Mature hERT induces  
 CC proliferation and/or differentiation of precursor or mature T cells  
 CC and is useful for promoting long-term in vitro culture of  
 CC T-lymphocytes and T-cell lines. It is used for treating  
 CC gastrointestinal diseases including peptic ulcer, colitis and  
 CC malignancy and for treating HIV infection.  
 CC  
 SQ Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 100.0%; Score 489; DB 17; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-116;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 ctaaaagatatttctaactgaagctgcatcattcattcattcattcattcattcatt 120  
 QY 121 GCAGGGCTCCCTAAACAGAACCAACTGGGTGATGATGATGATGATGATGATGAT 180  
 Db 121 gcagggtccctctaaacagaaagcaactgggtgaatgtaagtgattgaaaaaatt 180  
 QY 181 GAAGATCTTATTCATCTATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 Db 181 gaagatcttatcatcatcattgatacagatgactcttataatacagaatgtagtctcac 240  
 QY 241 CCCAGTGGACGATACACCAATGAAAGTCTTCTTGAGTGGACGATTTTTCACAT 300  
 Db 241 cccagttgaaggtatacagaatgagtgcttctcttgagttgcaagttattccacat 300  
 QY 301 GAGTCCGGAGATACACCAATGAAAGTCTTCTTGAGTGGACGATTTTTCACAT 360  
 Db 301 gactccggagatacagatattcatatgatacagtaagaaattctatccctagaacaac 360  
 QY 361 ATCTGTCTCTTAATGGAATATTAACAGATCTGATGCAAGAAATGAGAACTAGAG 420  
 Db 361 atctgtctcttcaatgaggaataatacagaatctgagtcgaagaatgtaggaactagag 420  
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 Db 421 gaaaaaaatattaaagaatttttgcagaggtttgtacatattgtccaaatgttcatcaac 480  
 QY 481 ACTTCTTGA 489  
 Db 481 acttcttga 489

RESULT 4  
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 ID AAT42242 standard; DNA; 489 BP.  
 AC AAT42242;  
 DT 05-FEB-1997 (first entry)  
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 DE Simian epithelium-derived T cell factor gene.  
 XX  
 KW Epithelium-derived T-cell factor; simian; human; culture; proliferation;  
 KW epithelial cell; differentiation; T-lymphocyte; African green monkey;  
 KW primer; PCR; polymerase chain reaction; amplification; probe; ss.

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XX OS Cercopithecus aethiops.
XX FH Key Location/Qualifiers
XX FT sig_peptide 1..144
XX FT mat_peptide /tag=a
XX FT 145..486
XX FT /*tag=b
XX PN US5552303-A.
XX PD 03-SEP-1996.
XX PF 08-MAR-1993; 93US-0031399.
XX PR 08-MAR-1993; 93US-0031399.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;
XX DR WPI: 1996-412063/41.
XX DR P-PSDB: AAM07254.
XX PT New isolated simian and human epithelium-derived T-cell factors -
XX PT T-lymphocytes and T-cell lines
XX PS Claim 21; Column 19-20; 22pp; English.
XX CC This is the nucleotide sequence encoding a simian epithelium-derived
XX CC T-cell factor (ETF). The protein was purified from African green monkey
XX CC CV-1 kidney cells in culture by conventional chromatography: hydrophobic,
XX CC anion exchange and reverse phase HPLC, followed by separation by
XX CC SDS-PAGE. The proteins from the SDS-PAGE were transferred to a PVDF
XX CC membrane and the bands corresp. to ETF was cut out for peptide sequencing.
XX CC Primers were synthesised based on this sequence and used to amplify a
XX CC 92 bp fragment from cDNA derived from CV-1/EBNA cells stimulated to
XX CC proliferate by phorbol 12-myristate 13-acetate. The 92 bp fragment was
XX CC labelled and used as a probe to isolate a clone c85.ETF which contained
XX CC this sequence. ETF is a protein of 15-17 kD which is expressed by
XX CC epithelial cells and stimulates proliferation and/or differentiation of
XX CC precursor and/or mature T cells. The protein is therefore useful for
XX CC promoting long term in vivo culture of T-lymphocytes and T-cell lines.
XX SQ Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 100.0%; Score 489; DB 17; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.3e-116;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACACCATTTGAGAGTATTTTCATCCAGTGTCTACTGTTTACTT 60
Db 1 atggaatttcgaaccacatttgagaagtatttccaccagtcctaccgtgttactt 60
QY 61 CTTAAGATCTATTTTCTAAGTGAAGCTGGCATTCATGCTTTCATTTGGGCTGTTTCACT 120
Db 61 ctaaaagatcatttctaaccgaagctgcatcattcattcatttggcgtttcagt 120
QY 121 GCAGGGCTCCCTAAACGAGACCACTGGGTGAATGTAATAAGATGTTGAAAAAATT 180
Db 121 gcaaggctccctaaacgaagcaccggtggaatgtaataagtgattgaaaaaatt 180
QY 181 GAAGATCTTATTCATATCATATGATGCTACTTATATTAAGAAAGATGTTTCACT 240
Db 181 gaagatcttattcaatcatatgatgatgctactctataacagaagatgattcact 240
QY 241 CCCAGTTGCAAGGTAACGACATGAAGTCTTCTTCTTGAAGTTGCAAGTATTTTCACT 300
Db 241 cccagttgcaaggtaacgacatgaagtccttctctctggaagttcgaagttatccat 300
QY 301 GAGTCGGAGATACAGATATTCATGATACAGTAAATCTTATCATCTGTAACAAAC 360

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Db 301 ggtccggagatcacatattccatgacagtagaataattcatctccatgaacaaac 360
QY 361 ATCTGTCTTCTTAATGGAATATACAGATCTGATGCAAAAGATGTAGAGAACTAGAG 420
Db 361 atctgtcttcttaatggagatataacagaatctcgatgcaagaagtgtgagactcagg 420
QY 421 GAAAAAATATTTAAGAAATTTTTCGAGAGTTTGTACATTTGTCCAAATGTTTCATCAG 480
Db 421 gaaaaaataattaaagaatttgcagagtttgtacatatgtgccaaatgttcacaaac 480
QY 481 ACTTCTTGA 489
Db 481 acttcttga 489

RESULT 5
AAT36634
ID AAT36634 standard; cDNA; 489 BP.
XX AC AAT36634;
XX DT 17-NOV-1996 (first entry)
XX DE Simian Interleukin-15 cDNA.
XX KM Interleukin-15; antagonist; mutein; graft versus host disease;
XX KM allograft; T-cell growth factor; ss.
XX OS Unspecified simian.
XX PN WO9626274-A1.
XX PD 29-AUG-1996.
XX PF 21-FEB-1996; 96WO-US02520.
XX PR 22-FEB-1995; 95US-0392317.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Grabstein KH, Paxton RJ, Pettit DK;
XX DR WPI: 1996-402367/40.
XX DR P-PSDB: AAR98526.
XX PT Antagonists of Interleukin-15 - are used to treat patients having
XX PT symptoms of graft-versus-host disease and for prolonging allo-graft
XX PT survival
XX PS Disclosure; Page 24; 32pp; English.
XX CC A cDNA clone (AAT36634) codes for simian Interleukin-15 (IL-15)
XX CC (AAR98526), a T-cell growth factor. Muteins of simian IL-15 or
XX CC human IL-15 (see also AAR98527) are useful as antagonists of IL-15
XX CC and can be prep. by PCR-mediated mutagenesis of the encoding
XX CC sequences. Preferred muteins have amino acid substitutions at
XX CC Asp56 and/or Glu156 of the IL-15 protein that prevent signal
XX CC transduction. They are useful for treating graft-versus-host
XX CC disease and for prolonging allograft survival.
XX SQ Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 100.0%; Score 489; DB 17; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.3e-116;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACACCATTTGAGAGTATTTTCATCCAGTGTCTACTGTTTACTT 60
Db 1 atggaatttcgaaccacatttgagaagtatttccaccagtcctaccgtgttactt 60
QY 61 CTTAAGATCTATTTTCTAAGTGAAGCTGGCATTCATGCTTTCATTTGGGCTGTTTCACT 120

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Db      61 ctaaagagcatctttctaactgaagctggcattcatttcttcaatttggcgtttcagtt 120
Qy      121 GCAGGCTCCCTAAAGACCAAGCAACTGGTGAATGTAATGATTTGAAAAAAT 180
Db      121 gaagggtccctaaacgaagcaactggtggaatgtataagattgaaaaaat 180
Qy      181 GAAGATCTTATTCATCTATGCAATATGATGCTACTTTATATACAGAAAGTGTTCAC 240
Db      181 gaagatcttattcaatctatgcatatgtcttacttatacagaagtgatgtcac 240
Qy      241 CCCAGTTCGAAGCTAACACCAATGAAGTCTTCTCTTGAGTGGCAAGTTATTCACAT 300
Db      241 cccagttgcaagtaacgaatgaagtgcttctctcttgagtgcaagttattcacat 300
Qy      301 GAGTCGGAGATACAGATATTCATGATACAGTGAAGAAATCTTATCATCTAGCAAAAC 360
Db      301 gagtcgagagatacagatattctatgatacagtagaataatcttactcctagaaacac 360
Qy      361 ATCTTGCTCTTATGGAATATACAGAAATCTGATGCAAAAGATGTGAGCACTAGAG 420
Db      361 atcttgcttctaattggaatatacagaatctggaatgcaagaatgtagaactagag 420
Qy      421 GAAAAAATATTAAGAAATTTTGCAGATTTTGTACATATTTGTCGAAATGTTCACTCAC 480
Db      421 gaaaaaataataaagaatttgcagagttctgtacataatgtccaaatgttccaaac 480
Qy      481 ACTTCTTGA 489
Db      481 acttcttga 489

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RESULT 6  
AAV02874  
ID AAV02874 standard; DNA; 489 BP.

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XX      AAV02874;
AC      08-MAY-1998 (first entry)
XX      Human epithelium derived T-cell factor DNA.
DE      Epithelium derived T-cell factor; ETF; human; gastrointestinal disease;
KW      B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;
XX      treatment; prevention; ss.
OS      Homo sapiens.
XX      Homo sapiens.
FH      Key
FT      CDS      Location/Qualifiers
FT      1..489
FT      /*tag= a
FT      /product= ETF
FT      1..144
FT      /*tag= b
FT      145..486
FT      /*tag= c
FT      /product= ETF
FT      /note= "Epithelium-derived T-cell factor"
XX      US5707616-A.
XX      13-JAN-1998.
XX      04-OCT-1996; 96US-0726817.
XX      22-FEB-1995; 95US-0393305.
XX      08-MAR-1993; 93US-0031399.
XX      22-APR-1994; 94US-0233606.
XX      (IMMUNEX CORP.
XX      Anderson DM, Eisenman JR, Fung V, Grabstein KH,
XX      Rauch C;
PI

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XX      WPT: 1998-100295/09.
DR      P-PSDB: AAM39187.
XX      Treatment or prevention of gastrointestinal diseases - by
PT      administering epithelium-derived T-cell factor polypeptide
XX      Claim 1C; Column 37-40; 34pp; English.
PS      This sequence encodes a human epithelium-derived T-cell factor (ETF)
XX      which is used in a method for treating or preventing gastrointestinal
CC      disease. These polypeptides have particular application in the treatment
CC      of gastrointestinal disorders associated with disruption of the
CC      gastrointestinal epithelium or villi such as chemotherapy and
CC      radiation therapy induced enteritis (gut toxicity), mucositis, peptic
CC      ulcer disease, gastroenteritis and colitis, villus atrophic disorders,
CC      malignancy and inflammatory bowel disease. ETF polypeptides may also be
CC      useful in the treatment of human immunodeficiency virus (HIV) and
CC      HIV-associated disease due to their ability to stimulate CD4+ and CD8+
CC      cells. Biologically active ETF may be used to treat a variety of other
CC      diseases or conditions where T-cell or B cell stimulation is desired.
XX      Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other:
SQ

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Query Match 100.0%; Score 489; DB 19; Length 489;  
Best Local Similarity 100.0%; Pred. No. 3.3e-116;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 ATGAGATTTTGAAGACACATTTGAGAGATTTTCCATCCAGTGCATCTGTTACTT 60
Db      1 atgagatttcgaacacacttggagagatttccatccagtcgaccgtgttactt 60
Qy      61 CTAAAGATCATTTTCTAAGTGAAGTGGCTATTCATGTTGGCTGTTTCACT 120
Db      61 ctaaagatcatttctaactgaagctggatcatgcttcttcttggtctgttca 120
Qy      121 GCAGGCTCCCTAAAGACCAAGCAACTGGGTGAAGTATTAAGTATTAAGTGAAAAAAT 180
Db      121 gcagggctccctaaacgaagcaactgggtgaagtaagtgattgaaaaaat 180
Qy      181 GAAGATCTTATTCATCTATGCAATATGATGCTACTTTATATACAGAAAGTGTTCAC 240
Db      181 gaagatcttattcaatctatgcatatgtatgcttacttatacagaagtgatgtcac 240
Qy      241 CCCAGTTCGAAGCTAACACCAATGAAGTCTTCTCTTGAGTGGCAAGTTATTCACAT 300
Db      241 cccagttgcaagtaacgaatgaagtgcttctcttgagtgcaagttattcacat 300
Qy      301 GAGTCGGAGATACAGATATTCATGATACAGTGAAGAAATCTTATCATCTAGCAAAAC 360
Db      301 gagtcgagagatacagatattctatgatacagtagaataatcttactcctagaaacac 360
Qy      361 ATCTTGCTCTTATGGAATATACAGAAATCTGATGCAAAAGATGTGAGCACTAGAG 420
Db      361 atcttgcttctaattggaatatacagaatctgatacagaatgtagaactagag 420
Qy      421 GAAAAAATATTAAGAAATTTTGCAGATTTTGTACATATTTGTCGAAATGTTCACTCAC 480
Db      421 gaaaaaataataaagaatttgcagagttctgtacataatgtccaaatgttccaaac 480
Qy      481 ACTTCTTGA 489
Db      481 acttcttga 489

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RESULT 7  
AAx29480  
ID AAx29480 standard; DNA; 489 BP.  
XX  
AC AAx29480;  
XX  
DT 10-JUN-1999 (first entry)

Human epithelium-derived T-cell factor (ETF) encoding DNA.

Epithelium-derived T-cell factor; ETF; immunoassay; enteritis; ulcer; T cell proliferation; gastrointestinal disease; mucositis; colitis; gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease; human immune deficiency virus; tumour; human; ss.

Homo sapiens.

US5892001-A.

06-APR-1999.

04-OCT-1996; 96US-0725969.

22-FEB-1995; 95US-0393305.

08-MAR-1993; 93US-0031399.

22-APR-1994; 94US-0233606.

04-OCT-1996; 96US-0725969.

(IMMUNEX CORP.

Anderson DM, Eisenman JR, Fung V, Grabstein KH; Rauch C;

WPI: 1999-253930/21.

P-PSDB: AAY03758, AAY03759.

Antibodies specific for epithelium-derived T-cell growth factor

Claim 1: Columns 37-40; 34pp; English.

The invention relates to an isolated antibody that binds specifically to a slamin or human epithelium-derived T-cell factor (ETF) polypeptide. The antibodies are used, optionally when immobilized or labeled, to detect and quantify ETF in standard immunoassays. They may also be used as diagnostic and therapeutic agents, e.g. when conjugated to toxins (or their precursors) or radionuclides. ETF induces proliferation and/or differentiation of T cells (or their precursors), e.g. for use in establishing long term in vitro cultures; and is also used to treat gastrointestinal disease (e.g. enteritis or mucositis induced by chemotherapy or radiation, peptide ulcer, gastroenteritis, colitis, villus atrophy, malignancy and inflammatory bowel disease), to treat human immune deficiency virus infection or associated disease, or generally in any situation requiring stimulation of T or B cell proliferation, secretion of immunoglobulins or certain cytokines, increased anti-infectious disease immunity, induction of T-cell lytic activity or increased destruction of tumour or virus-infected cells. The present sequence represents a DNA encoding a human ETF precursor polypeptide sequence.

Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 100.0%; Score 489; DB 20; Length 489;

Best Local Similarity 100.0%; Pred. No. 3.3e-116;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0

1 ATGACAATTTGGAAACACACATTGGAGAACTATTTCATCAGTGTCTTTACTT 60  
|||||  
1 atggaatttcgaaacacacattggaagtatttcacatccagtcgactcgttactt 60  
61 CTAAAGACTCATTTTCTTAACGTGACATGTCATTCATGTTTGGCGTTTCACT 120  
62 ctaaagactcatttcttaactcgaagctgcatcattccattcatttggcgttccagt 120  
63 121 GCAGGCGTCCCTAAAGACGAACCACTGGTGTAATGTAAGTATTGAAAAAATT 180  
64 121 gcaggcgctccctaaagacgaacccaactgggtgaatgtataagtgattgaaaaaatt 180  
65 181 GAAGATCTTATTCATCATGATGATTTGATGCTACTTTATATACGAAGAAGTATGTCAC 240  
|||||

Db	181	gaagctctatccaatcattatgcatatgctacttataatacgaagaatgtaatgtccac	2400
OY	241	CCCACTTCGAGGTAAACGCAATGAAGTCTTCTCTTGGAGTTGCAAGTATTATTCACAT	3000
Db	241	cccccttgcagaagttaacgcgaatgaagtgcttctccttgagtgcagaattatccaat	3000
OY	301	GAGTCCGAGATACAGATTATTCATGATACAGTAGAATAATCTTATCATCTTCAGCAACAAC	3600
Db	301	gagtcgcgaggtacagatattcatcatgatacagtagaatacttcatcatccctcagaanaaac	3600
OY	361	ATCTTGCTTCTTAATGGGAATATATAACGAATCTTGATGCGAAAGAAATGTGAGCAACTAGAG	4200
Db	361	atcttgcttcttaatgggaataataatacagaatcttgcagaagaatgttgaggaactagag	4200
OY	421	GAAGAAAAATATTAAGAATTTTTCGACAGTTTGTACATATTTGCCAAATGTTTCATCAAC	4800
Db	421	gaagaaaaatattaaagaatttttcgcagagttttgtataatgtccaaatgttcatcaac	4800
OY	481	ACTTCTTGA 489	
Db	481	acttcttga 489	

XX	AAZ90031
XX	AAZ90031 standard; cDNA; 489 BP.
AC	AAZ90031;
DT	09-MAY-2000 (first entry)
XX	
DE	Slimian interleukin-15 (IL-15) nucleotide sequence.
XX	
KW	Interleukin-15; IL-15; antagonist; irritable bowel disease; IBD;
KM	celiac disease; treatment; ss.
XX	
OS	Primate.
XX	
PN	WO200002582-A2.
PD	20-JAN-2000.
XX	
PF	09-JUL-1999; 99WO-GB02201.
XX	
PR	10-JUL-1998; 98GB-0014892.
PA	(KENN-) KENNEDY INST RHEUMATOLOGY MATHILDA & TER.
XX	
PI	Londel M, Quaratino S, Maiuri L;
DR	WP1: 2000-171080/15.
DR	P-PADB; AAT78594.
PT	
PT	Use of antagonists of Interleukin-15 for treating an inflammatory bowel
XX	disease, particularly celiac disease
PS	-
XX	Disclosure; Page 70; 70pp; English.
CC	This sequence represents the simian interleukin 15 (IL-15) nucleotide
CC	sequence. The IL-15 nucleotide sequence and the protein encoded by it can
CC	be used to determine and create antagonists of IL-15. An antagonist of
CC	IL-15 can be used for treating an inflammatory bowel disease (IBD). The
CC	invention relates to the treatment of celiac disease using IL-15
CC	antagonists. The antagonists are preferably mutants of IL-15, antibodies
CC	against IL-15 or IL-15 molecules bound to chemical groups that interfere
CC	with the ability of IL-15 to effect a signal transduction through either
CC	the alpha or the gamma subunit of the IL-15 receptor complex. The IL-15
CC	antagonists of the invention can be used to treat irritable bow disease
CC	especially celiac disease.
XX	
XX	Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 100.0%; Score 489; DB 21; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-116;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTCGAAACACATTTGAGAAGTATTCATCCAGCTGCTACTGTGTTACTT 60  
 |||||||  
 Db 1 atggaatttcgaacacacatttgaagaatttccaccagctgctactgttactt 60

QY 61 CTAAGAAGTCATTTTCTTAAGTGAAGCGCATTCATGCTTCATTTGGCGTTTCAGT 120  
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 Db 61 ctaagaagtcatttcttaactgaagcgtggcatcattcttcatcttggcgttccagt 120

QY 121 GCAGGGCTCCCTAAACAGAACCCACTGGGTGAATGAATGAATGATTTGAAAAAAT 180  
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 Db 121 gcagggtcccttaaacagaagccaactgggtgaatgaatgaattgttgaaaaaatt 180

QY 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 |||||||  
 Db 181 gaagatcttattcatctatcatatgatatgatatgatatgatatgatatgatatg 240

QY 241 CCCAGTTGCAAGGTACAGCAATGAGTCTTCTGTTGAGTTCAGATTTATTTCAAT 300  
 |||||||  
 Db 241 cccagttgcaaggtacagcaatgagtccttcttggagttgcaagttatctacat 300

QY 301 GAGTCGAGATACAGATTTATTCATGATGATGATGATGATGATGATGATGATGAT 360  
 |||||||  
 Db 301 gagtcgagatagatattcatgatacagtagaataatctatcatctctgcaaacac 360

QY 361 ATCTTGCTTCTTATGGAATATTAAGATCTGATGATGATGATGATGATGATGAT 420  
 |||||||  
 Db 361 atcttgcttcttcaatggaatataacagaaatctgatacagaaatgtagaactag 420

QY 421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTTGCCAATGTCATCAAC 480  
 |||||||  
 Db 421 gaaaaaataataagaatttttcagagtttgcagagtttgcataatgccaaatgtcat 480

QY 481 ACTTCTTGA 489  
 |||||||  
 Db 481 acttcttga 489

RESULT 9  
 AAZ38245  
 ID AAZ38245 standard; CDNA; 489 BP.  
 XX  
 AC AAZ38245;  
 XX  
 DT 09-FEB-2000 (first entry)  
 XX  
 DE Human epithelium-derived T-cell factor (ETF) cDNA.  
 XX  
 KW ETF: epithelium-derived T-cell factor; T-cell; T-lymphocyte;  
 KW proliferation; differentiation; growth factor; precursor; mature; CD4+;  
 KW CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;  
 KW gastrointestinal disease; gastroenteritis; colitis;  
 KW inflammatory bowel disease; villus atrophic disorder; enteritis;  
 KW chemotherapy; radiotherapy; gut toxicity; cancer; side effect;  
 KW tolerated dose; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..489  
 FT /\*tag= a  
 FT /product= "Human ETF precursor protein (AAV52310)"  
 FT 1..144  
 FT sig\_peptide  
 FT /\*tag= b  
 FT mat\_peptide 145..489  
 FT /\*tag= c  
 FT /product= "Mature human ETF (AAV52311)"  
 XX  
 XX US5985262-A.  
 XX

PD 16-NOV-1999.  
 XX  
 PF 03-FEB-1997; 97US-0794524.  
 XX  
 PR 22-FEB-1995; 95US-0393305.  
 PR 04-OCT-1996; 96US-0726817.  
 PR 08-MAR-1993; 93US-0031399.  
 PR 22-APR-1994; 94US-0233606.  
 XX  
 PA (IMM) IMMUNEX CORP.  
 XX  
 PI Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;  
 DR WPI: 2000-022267/02.  
 DR P-PSDB: AAV52310, AAV52311.  
 XX  
 XX Stimulation of T-cells in human immunodeficiency virus infected  
 PT patients -  
 PS Claim 1; Columns 37-40; 33pp; English.

This sequence represents human epithelium-derived T-cell factor (ETF) cDNA. ETF is a previously unidentified T-cell growth factor which stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to proliferate and differentiate. It also promotes proliferation of the gastrointestinal epithelium. The protein can be used to promote long-term in vitro culture of T-lymphocytes and T-cell lines. ETF can be used for treating HIV infection, HIV-associated diseases, and other diseases or conditions where stimulation of T-cell proliferation would be desirable e.g., it could be used to augment the destruction of tumour cells or virally-infected cells. ETF may also be used to treat or prevent gastrointestinal disease, including chemotherapy and radiotherapy associated enteritis, gastroenteritis, colitis, inflammatory bowel disease and villus atrophic disorders. Chemotherapy and radiotherapy associated enteritis (gut toxicity) results in bleeding and sepsis due to gastrointestinal flora entering the blood, and thus can limit the dosage of therapeutic agent administered to a cancer patient. ETF may therefore be used to increase the tolerated doses radiotherapy and chemotherapy.

Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 100.0%; Score 489; DB 21; Length 489;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-116;  
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAATTCGAAACACATTTGAGAAGTATTCATCCAGCTGCTACTGTGTTACTT 60  
 |||||||  
 Db 1 atggaatttcgaacacacatttgaagaatttccaccagctgctactgttactt 60

QY 61 CTAAGAAGTCATTTTCTTAAGTGAAGCGCATTCATGCTTCATTTGGCGTTTCAGT 120  
 |||||||  
 Db 61 ctaagaagtcatttcttaactgaagcgtggcatcattcttcatcttggcgttccagt 120

QY 121 GCAGGGCTCCCTAAACAGAACCCACTGGGTGAATGAATGAATGATTTGAAAAAAT 180  
 |||||||  
 Db 121 gcagggtcccttaaacagaagccaactgggtgaatgaatgaattgttgaaaaaatt 180

QY 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
 |||||||  
 Db 181 gaagatcttattcatctatcatatgatatgatatgatatgatatgatatgatatg 240

QY 241 CCCAGTTGCAAGGTACAGCAATGAGTCTTCTGTTGAGTTCAGATTTATTTCAAT 300  
 |||||||  
 Db 241 cccagttgcaaggtacagcaatgagtccttcttggagttgcaagttatctacat 300

QY 301 GAGTCGAGATACAGATTTATTCATGATGATGATGATGATGATGATGATGATGAT 360  
 |||||||  
 Db 301 gagtcgagatagatattcatgatacagtagaataatctatcatctctgcaaacac 360

QY 361 ATCTTGCTTCTTATGGAATATTAAGATCTGATGATGATGATGATGATGATGAT 420  
 |||||||  
 Db 361 atcttgcttcttcaatggaatataacagaaatctgatacagaaatgtagaactag 420

QY 421 GAAAAAATATTAAAGATTTTTCAGAGTTTGTACATATTGTCACAAATGTTTCATCAAC 480  
DB 421 gaaaaaaatattaaagaatttttcgaggtttgtacatatgtgccaaatgttcatcaac 480  
QY 481 ACTTCTTGA 489  
DB 481 acttcttga 489  
RESULT 10  
AAE57018  
ID AAE57018 standard; cDNA; 489 BP.  
XX AAE57018;  
AC AAE57018;  
XX 14-MAY-2001 (first entry)  
DE Human ETF (hETF) polypeptide encoding cDNA.  
XX  
XX Epithelium-derived T-cell factor; ETF; simian; human; enteritis;  
KW gastrointestinal disease; mucositis; peptic ulcer; cytostatic;  
KW villus atrophic disorder; inflammatory bowel disease; antiinflammatory;  
KW anti-HIV; antiviral; T-lymphocyte stimulator; ss.  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH CDS 1..489  
FT /\*tag= a  
FT /\*product= "hETF"  
FT sig\_peptide 1..144  
FT /\*tag= b  
FT mat\_peptide 145..486  
FT /\*tag= C  
FT /\*note= "specifically claimed (see AAB62015)"  
XX  
XX US6184359-B1.  
PN 06-FEB-2001.  
XX  
XX 09-NOV-1998; 98US-0189193.  
PR 22-FEB-1995; 95US-0393305.  
PR 04-OCT-1996; 96US-0725969.  
PR 08-MAR-1993; 93US-0031399.  
PR 22-APR-1994; 94US-0233606.  
XX  
XX (IMMV ) IMMUNEX CORP.  
XX  
XX Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;  
PI WPI: 2001-217801/22.  
XX P-PSDB; AAB62014, AAB62015.  
DR  
XX  
XX New antibodies that specifically binds epithelium-derived T-cell factor  
PT polypeptide useful for e.g. treating or preventing gastrointestinal  
PT diseases, HIV and HIV-associated diseases, augmenting destruction of  
PT tumour cells -  
XX  
XX Claim 1; Column39-40; 35pp; English.  
XX  
XX The invention relates to simian and human epithelium-derived T-cell  
CC factor (ETF) polypeptides. Antibodies that specifically bind to the ETF  
CC polypeptides are used for treating or preventing gastrointestinal  
CC diseases, such as chemotherapy and radiation therapy-induced enteritis  
CC and mucositis, peptic ulcer disease, villus atrophic disorders and  
CC inflammatory bowel disease; for increasing tolerated doses for radiation  
CC therapy and chemotherapy agents which are limited by gastrointestinal  
CC toxicity; and for treating HIV and HIV-associated diseases. The  
CC antibodies are further used to treat a variety of other diseases or  
CC conditions where it is desired to stimulate proliferation of  
CC T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B

CC lymphocytes, to augment anti-infectious disease immunity, to induce CTL,  
CC LAK or NK lytic activity, or to augment the destruction of tumour cells  
CC or cells infected with virus. The present sequence represents a cDNA  
CC encoding the human ETF (hETF) polypeptide.  
XX  
SQ Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;  
Query Match 100.0%; Score 489; DB 22; Length 489;  
Best Local Similarity 100.0%; Pred. No. 3,3e-116;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGAGATTTTGAAGACACATTTGAGAGTATTTCATCCAGTGCATCTGTTTACTT 60  
DB 1 atgagatttcgaaccacatttgagaagatttccatccagtcacccgttcttactt 60  
QY 61 CTAAAGATCATTTTCTTAAGTGAAGTGCATTCATGCTCTTCAATTTTGGCTTTTCAGT 120  
DB 61 ctaaaagatcattttcttaactgaagctggcatcattcattcttcttggctgttcaagt 120  
QY 121 GCAGGCTCCCTAAACAGACCACTGGGTGAATGATTAAGTGAATAAATTT 180  
DB 121 gcaggctccctaaacagaccagcaactgggtgaatgaatgaatgaatgaatgaatgaat 180  
QY 181 GAAGATCTTAATTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
DB 181 gaagatcttatttcaatctatgatactgattgattgattgattgattgattgattgattgatt 240  
QY 241 CCCAGTTGCAAGTATACAGCAATGAAGTGTCTTCTTGTGAGTTGCAAGTATTTCACAT 300  
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QY 301 GAGTCCGAGATPACAGATTTTCATGATACAGTGAATAATCTTATCCATGCAAAACAC 360  
DB 301 gagtcggagatcacagatttcatgatacagtagaataatcttcttccatgcaaaacac 360  
QY 361 ATCTTGTCTTGAATGAGATATACAGATCTGATGCAAAAGTGAAGATGAGATGAGATGAGAT 420  
DB 361 atcttgtcttctaagtgagatacagaaatctgagtagcaagaatgtaggagaaatcagag 420  
QY 421 GAAAAAATATTAAAGATTTTTCAGAGTTTGTACATATTGTCACAAATGTTTCATCAAC 480  
DB 421 gaaaaaaatattaaagaatttttcgaggtttgtacatatgtgccaaatgttcatcaac 480  
QY 481 ACTTCTTGA 489  
DB 481 acttcttga 489  
RESULT 11  
AAT00526  
ID AAT00526 standard; cDNA; 489 BP.  
XX AAT00526;  
AC AAT00526;  
XX  
XX 02-FEB-1996 (first entry)  
DE Human interleukin-15 precursor.  
XX  
XX Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH CDS 1..489  
FT /\*tag= a  
FT /\*note= "Claimed"  
FT misc\_feature 145..489  
FT /\*tag= b  
FT /\*note= "Claimed"  
XX  
XX W09527722-A.



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QY 121 GCAGGCTCCCTAAACAGACCAAGCTGGTGAATGTAATGATTTGAAAAAATT 180
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Db 121 gcaggctccctaaacagacccaactgggtgaatgtaattgtaaaatc 180
QY 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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Db 241 cccagtgcaagatgaagcaagcaagcaagcaagcaagcaagcaagcaagcaagca 300
QY 301 GAGTCGGAGATACAGATATTCATGATGATGATGATGATGATGATGATGATGATGAT 360
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Db 301 gagtcggagatgacagatcatcatcatcatcatcatcatcatcatcatcatcatcat 360
QY 361 ATCTGTCTTCTAATGGAATATACAGATCTGATGATGATGATGATGATGATGATGAT 420
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Db 361 agttgtcttctaaatggaatgtaacagaaatcctgagatgcaagaaatgtagaactg 420
QY 421 GAAAAAATATTAAGCAATTTTGCAGAGTTTGTACATATTTGCCAAATGTCATCAAC 480
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Db 421 gaaaaaatatttaagaatatttgcagagatttgcatacatatgccaaatgtaacaaac 480
QY 481 ACTTCTTGA 489
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Db 481 acttcttga 489

RESULT 13
AAT49455
ID AAT49455 standard; cDNA; 489 BP.
XX
AC AAT49455;
XX
DT 11-MAR-1997 (first entry)
XX
DE Simian epithelium derived T cell factor cDNA.
XX
KW SETF; African green monkey; CV1/EBNA cell; T-cell; B-cell;
   lymphocyte; proliferation; differentiation; gastrointestinal;
   HIV infection; human immunodeficiency virus; ss.
XX
OS Cercopithecus aethiops.
XX
FH Key
FT CDS
FT mat_peptide
FT /tag= a
FT /tag= b
FT /product= SETF
XX
PN US574138-A.
XX
PD 12-NOV-1996.
XX
PE 08-MAR-1993; 93US-0031399.
XX
PR 22-FEB-1995; 95US-0393305.
PR 08-MAR-1993; 93US-0031399.
PR 22-APR-1994; 94US-0233606.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI Rauch C;
XX
DR WPI: 1996-517923/51.
DR P-PSDB; AAM09098 AND AAM09099.
XX
PT New epithelium derived T cell factor - induces proliferation of T
   and B cells, stimulates destruction of tumour and virus-infected
   cells and protects against toxicity, partic. for treating intestinal

```

```

PT disease and HIV infection
XX
PS Claim 1; Fig 1; 35pp; English.
XX
CC The simian ETF (epithelium derived T cell factor) was isolated from
CC African green monkey CV1/EBNA cell conditioned medium. The N-
CC terminal sequence of the purified SETF was determined and then PCR
CC primers were designed based on the sequence information. A 92 bp
CC fragment was amplified from CV1/EBNA DNA and was used as a probe to
CC screen a CV1/EBNA cDNA library for the full-length SETF coding
CC sequence (i.e. the present sequence). Mature SETF induces
CC proliferation and/or differentiation of precursor or mature T cells
CC and is useful for promoting long-term in vitro culture of
CC T-lymphocytes and T-cell lines. It is used for treating
CC gastrointestinal diseases including peptic ulcer, colitis and
CC malignancy and for treating HIV infection.
XX
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

```

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Query Match 95.1%; Score 465; DB 17; Length 489;
Best Local Similarity 96.9%; Pred. No. 4,8e-110;
Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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QY 1 ATGGAATTTGGAACCAATTTGAGAAATTTCCATGCTACCTGTTTACTT 60
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Db 61 ctaaacagtcatttcttaacatgagctgcatcattcatcttcttcttcttcttctt 120
QY 121 GCAGGCTCCCTAAACAGACCAAGCTGGTGAATGTAATGATTTGAAAAAATT 180
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Db 121 gcaggctccctaaacagacccaactgggtgaatgtaattgtaaaatc 180
QY 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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Db 181 gaagatcttattcatatcatatcatatcatatcatatcatatcatatcatatcat 240
QY 241 CCCAGTTCAGAGTACAGACCAATGATGATGATGATGATGATGATGATGATGATGATGAT 300
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QY 361 ATCTGTCTTCTAATGGAATATTAAGCAATTTTGCAGAGTTTGTACATATTTGCCAAATGTCATCAAC 420
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 agttgtcttctaaatggaatgtaacagaaatcctgagatgcaagaaatgtagaactg 420
QY 421 GAAAAAATATTAAGCAATTTTGCAGAGTTTGTACATATTTGCCAAATGTCATCAAC 480
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 gaaaaaatatttaagaatatttgcagagatttgcatacatatgccaaatgtaacaaac 480
QY 481 ACTTCTTGA 489
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 acttcttga 489

RESULT 14
AAT42243
ID AAT42243 standard; DNA; 489 BP.
XX
AC AAT42243;
XX
DT 05-FEB-1997 (first entry)
XX
DE Human epithelium-derived T cell factor gene.
XX
KW Epithelium-derived T-cell factor; simian; human; culture; proliferation;
   epithelial cell; differentiation; T-lymphocyte; African green monkey;

```

KM primer; PCR; polymerase chain reaction; amplification; probe; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT sig\_peptide 1..144  
 FT mat\_peptide /\*tag= a  
 FT 145..486  
 FT /\*tag= b  
 XX  
 XX US5552303-A.  
 XX  
 XX 03-SEP-1996.  
 XX  
 XX 08-MAR-1993; 93US-0031399.  
 XX  
 XX 08-MAR-1993; 93US-0031399.  
 XX  
 XX (IMMV ) IMMUNEX CORP.  
 XX  
 XX Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;  
 XX WPI: 1996-412063/41.  
 XX P-PSDB: AAM07255.  
 XX  
 XX New isolated simian and human epithelium-derived T-cell factors -  
 XX T-lymphocytes and T-cell lines  
 XX  
 XX Claim 21: Column 23-24; 22pp; English.  
 XX  
 CC This is the nucleotide sequence encoding a human epithelium-derived  
 CC T-cell factor (ETF). The gene was obtained using a 1.37 kb fragment of  
 CC the corresp. African green monkey gene (AAT42242) as a probe to screen a  
 CC cDNA library constructed from RNA derived from the IMVH cell line.  
 CC This cell line is derived by stable transformation of a human bone  
 CC marrow stromal cell culture with pSVneo. From a pool of about 1000 cDNA  
 CC clones, one clone 141.hetr contained this sequence. ETF is a protein of  
 CC 15-17 kD which is expressed by epithelial cells and stimulates  
 CC proliferation and/or differentiation of precursor and/or mature T cells.  
 CC The protein is therefore useful for promoting long term in vivo culture  
 CC of T-lymphocytes and T-cell lines.  
 CC  
 CC Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;  
 SO  
 Query Match 95.1%; Score 465; DB 17; Length 489;  
 Best Local Similarity 96.9%; Pred. No. 4.8e-110;  
 Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 ATGAGATTTCGAAACACATTTGAGAGATTTTCATCGACGTGCTGTTTACTT 60  
 DB 1 atgagaatttcgaacacatttgagaagatttcacatccagtcgtacttggttactt 60  
 QY 61 CTAAGAGTCATTTTCTAAGTCAGAGCGGATTCATGTCCTTCAATTTGGCTGTTTCACT 120  
 DB 61 ctaaacagtcatttctcaactgaagcgcgcatcagtcctcatttggcgtgttcaagt 120  
 QY 121 GCGAGGCTCCCTAAACAGAGCCCACTGGGTGAATGAATGAATGAATGAATGAAT 180  
 DB 121 gcagggctctcctaacaacagagccaactgggtgaatgaatgaatgaatgaatgaat 180  
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 DB 181 gaagatcttctcaatctatgacatattgacttcttatacgaagaagtgaattcact 240  
 QY 241 CCCAGTTCAAGGTATACAGCAATGAAGTCTTCTCTTGAGTGGCAAGTATTTTCAT 300  
 DB 241 cccagttgcaaggtataacgaagaagtgccttctcttgagttacaagaatttcaact 300  
 QY 301 GAGTCCGGAATACAGATATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 360  
 DB 301 gagtcgcgaagatgcaagattctatgacagtagaanaatctgcatcctcagcaacaac 360

QY 361 ATCTTGCTCTGATATGGAATATTAACAGAAATCTGCATCCAAAGATGTGAGCACTAGAC 420  
 DB 361 agttgtcttctcaatggaagaaatctgacatctgacgaagaatgtagaactgag 420  
 QY 421 GAAAAAATATTAAGAAATTTTGCAGGTTTGTACATATTTGCCAAATGTTTATCAAC 480  
 DB 421 gaaaaaataataaagaatttgcagagtttgcagatttgcacattgtccaaatgtcatcaac 480  
 QY 481 ACTTCTTGA 489  
 DB 481 actctctga 489  
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 AAT36635  
 ID AAT36635 standard; cDNA; 489 BP.  
 XX  
 XX AAT36635;  
 XX  
 XX 17-NOV-1996 (first entry)  
 XX  
 XX Human interleukin-15 cDNA.  
 XX  
 KM Interleukin-15; antagonist; mutein; graft versus host disease;  
 KM allograft; T-cell growth factor; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9626274-A1.  
 XX  
 XX 29-AUG-1996.  
 XX  
 XX 21-FEB-1996; 96WO-US02520.  
 XX  
 XX 22-FEB-1995; 95US-0392317.  
 XX  
 XX (IMMV ) IMMUNEX CORP.  
 XX  
 XX Grabstein KH, Paxton RJ, Pettit DK;  
 XX WPI: 1996-402367/40.  
 XX P-PSDB: AAR98527.  
 XX  
 PT Antagonists of interleukin-15 - are used to treat patients having  
 PT symptoms of graft-versus-host disease and for prolonging allo:graft  
 PT survival  
 PS Disclosure; Page 25; 32pp; English.  
 XX  
 CC A cDNA clone (AAT36635) codes for human interleukin-15 (IL-15)  
 CC (AAR98527), a T-cell growth factor. Muteins of human IL-15 or  
 CC simian IL-15 (see also AAR98526) are useful as antagonists of IL-15  
 CC and can be prepd. by PCR-mediated mutagenesis of the encoding  
 CC sequences. Preferred muteins have amino acid substitutions at  
 CC Asp56 and/or Gln156 of the IL-15 protein that prevent signal  
 CC transduction. They are useful for treating graft-versus-host  
 CC disease and for prolonging allograft survival.  
 CC  
 CC Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;  
 SO  
 Query Match 95.1%; Score 465; DB 17; Length 489;  
 Best Local Similarity 96.9%; Pred. No. 4.8e-110;  
 Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 ATGAGATTTCGAAACACATTTGAGAGATTTTCATCGACGTGCTGTTTACTT 60  
 DB 1 atgagaatttcgaacacatttgagaagatttcacatccagtcgtacttggttactt 60  
 QY 61 CTAAGAGTCATTTTCTAAGTCAGAGCGGATTCATGTCCTTCAATTTGGCTGTTTCACT 120  
 DB 61 ctaaacagtcatttctcaactgaagcgcgcatcagtcctcatttggcgtgttcaagt 120

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Db 121 gcaaggctccctaacaagcaacggaacggaagcgaatgaatgaatgaatgaatgaatgaat 180
QY 181 GAAGATCTTATTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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Db 181 gaagatcttatcatctatctatctatctatctatctatctatctatctatctatctatct 240
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QY 301 GAGTCGGAGATACAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
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    | ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
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QY 421 GAAAAAATATTAAAGATTTTTCAGAGTTCATATTTGTCATATTTGTCATATTTGTCAT 480
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Db 421 gaaaaaatattaaagatlttgcagaglttgcagaglttgcagaglttgcagaglttgcag 480
QY 481 ACTTCTTGA 489
    |||||||
Db 481 acttcttga 489
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Job time: 2794 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2002, 23:32:52 ; Search time 60.38 Seconds  
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Title: US-09-724-841-1

Perfect score: 489  
Sequence: 1 ATGAGATTTCGAAACACCA.....TGTTCAACACACTTCTTGA 489

Scoring table: IDENTITY\_NUC  
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Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	489	100.0	489	1 US-08-031-399-4	Sequence 4, Appl1
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3	489	100.0	489	1 US-08-535-733-1	Sequence 1, Appl1
4	489	100.0	489	1 US-08-726-817-1	Sequence 1, Appl1
5	489	100.0	489	1 US-08-504-042-4	Sequence 4, Appl1
6	489	100.0	489	1 US-08-392-317B-2	Sequence 2, Appl1
7	489	100.0	489	2 US-08-725-969-1	Sequence 1, Appl1
8	489	100.0	489	2 US-08-794-524-1	Sequence 1, Appl1
9	489	100.0	489	3 US-08-134-132-2	Sequence 2, Appl1
10	489	100.0	489	4 US-09-134-134A-2	Sequence 2, Appl1
11	489	100.0	489	4 US-09-134-456-2	Sequence 2, Appl1
12	489	100.0	489	4 US-09-196-427-2	Sequence 2, Appl1
13	489	100.0	489	4 US-09-189-193-1	Sequence 1, Appl1
14	489	100.0	489	5 PCT-US94-03793-4	Sequence 4, Appl1
15	489	100.0	489	5 PCT-US96-06423-1	Sequence 1, Appl1
16	489	100.0	1202	3 US-08-962-503-11	Sequence 11, Appl1
17	487.4	99.7	489	3 US-08-842-947-5	Sequence 5, Appl1
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20	465	95.1	489	1 US-08-393-305-4	Sequence 4, Appl1
21	465	95.1	489	1 US-08-726-817-4	Sequence 4, Appl1
22	465	95.1	489	1 US-08-504-042-1	Sequence 1, Appl1
23	465	95.1	489	1 US-08-392-317B-1	Sequence 1, Appl1
24	465	95.1	489	2 US-08-725-969-4	Sequence 4, Appl1
25	465	95.1	489	2 US-08-794-524-4	Sequence 4, Appl1
26	465	95.1	489	3 US-09-134-132-1	Sequence 1, Appl1
27	465	95.1	489	4 US-09-134-134A-1	Sequence 1, Appl1

28	465	95.1	489	4 US-09-134-456-1	Sequence 1, Appl1
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42	325.8	66.6	345	3 US-08-842-947-3	Sequence 3, Appl1
43	45.6	9.3	60	3 US-09-251-645-11	Sequence 11, Appl1
44	37.8	7.7	37948	1 US-08-158-232-42	Sequence 42, Appl1
45	36.6	7.5	3660	1 US-08-158-232-42	Sequence 42, Appl1

#### ALIGNMENTS

RESULT 1  
: Sequence 4, Application US/08031399  
: Patent No. 5552303  
: GENERAL INFORMATION:  
: APPLICANT: Grabstein, Kenneth  
: APPLICANT: Anderson, Dirk  
: APPLICANT: Eisenman, June  
: APPLICANT: Fung, Victor  
: APPLICANT: Rauch, Charles  
: TITLE OF INVENTION: Epithelium-derived T-cell factor  
: NUMBER OF SEQUENCES: 12  
: CORRESPONDENCE ADDRESSES:  
: ADDRESSEE: Immunex Corporation  
: STREET: 51 University Street  
: CITY: Seattle  
: STATE: Washington  
: COUNTRY: USA  
: ZIP: 98101  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: PatentIn Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/031,399  
: FILING DATE: 19930308  
: CLASSIFICATION: 530  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Launer, Charlene  
: REGISTRATION NUMBER: 33,035  
: REFERENCE/DOCKET NUMBER: 2811  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 206-587-0430  
: INFORMATION FOR SEQ ID NO: 4:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 489 base pairs  
: TYPE: NUCLEIC ACID  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: cDNA  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 1..489  
: US-08-031-399-4

Query Match 100.0% ; Score 489 ; DB 1 ; length 489 ;  
Best Local Similarity 100.0% ; Pred. No. 1.6e+124 ; Indels 0 ; Gaps 0 ;  
Matches 489 ; Conservative 0 ; Mismatches 0 ;

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QY 1 ATGAGATTTCGAACACATTTGAGAGATTTCATCCAGTCTACTGTGTTACTT 60
DB 1 ATGAGATTTCGAACACATTTGAGAGATTTCATCCAGTCTACTGTGTTACTT 60
QY 61 CTAAACAGTCATTTTCTAACTGAGTGGCATTCATGCTTTCATTTGGGCTGTTTACT 120
DB 61 CTAAACAGTCATTTTCTAACTGAGTGGCATTCATGCTTTCATTTGGGCTGTTTACT 120
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DB 121 GCAGGCTTCTTAAACAGACCACTGGGTGATGTAATAGTGAATTTGAAAAAAT 180
QY 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 CCCAGTTCGAAGTACAGCAATGAGTCTTCTCTGAGTTCACAAGTTATTTGACTT 300
DB 241 CCCAGTTCGAAGTACAGCAATGAGTCTTCTCTGAGTTCACAAGTTATTTGACTT 300
QY 301 GAGTCCGAGATGCAAGTATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 GAGTCCGAGATGCAAGTATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 AGTTGCTCTTCTAATGGAATGTACAGATCTGATGCAAAAGATGTGAGCAATGAG 420
DB 361 AGTTGCTCTTCTAATGGAATGTACAGATCTGATGCAAAAGATGTGAGCAATGAG 420
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCAAAATGTTCAATCAAC 480
DB 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCAAAATGTTCAATCAAC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 2
US-08-393-305-1
; Sequence 1, Application US/08393305
; Patent No. 5574138
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,305
; FILING DATE: 22-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 1:
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SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: 1..489
; US-08-393-305-1

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACATTTGAGAGATTTCATCCAGTCTACTGTGTTACTT 60
DB 1 ATGAGATTTCGAACACATTTGAGAGATTTCATCCAGTCTACTGTGTTACTT 60
QY 61 CTAAACAGTCATTTTCTAACTGAGTGGCATTCATGCTTTCATTTGGGCTGTTTACT 120
DB 61 CTAAACAGTCATTTTCTAACTGAGTGGCATTCATGCTTTCATTTGGGCTGTTTACT 120
QY 121 GCAGGCTTCTTAAACAGACCACTGGGTGATGTAATAGTGAATTTGAAAAAAT 180
DB 121 GCAGGCTTCTTAAACAGACCACTGGGTGATGTAATAGTGAATTTGAAAAAAT 180
QY 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 CCCAGTTCGAAGTACAGCAATGAGTCTTCTCTGAGTTCACAAGTTATTTGACTT 300
DB 241 CCCAGTTCGAAGTACAGCAATGAGTCTTCTCTGAGTTCACAAGTTATTTGACTT 300
QY 301 GAGTCCGAGATGCAAGTATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 360
DB 301 GAGTCCGAGATGCAAGTATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 AGTTGCTCTTCTAATGGAATGTACAGATCTGATGCAAAAGATGTGAGCAATGAG 420
DB 361 AGTTGCTCTTCTAATGGAATGTACAGATCTGATGCAAAAGATGTGAGCAATGAG 420
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCAAAATGTTCAATCAAC 480
DB 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCAAAATGTTCAATCAAC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 3
US-08-535-733-1
; Sequence 1, Application US/08535733
; Patent No. 5660824
; GENERAL INFORMATION:
; APPLICANT: Quinn, Lebris
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Trout, Anthony B.
; TITLE OF INVENTION: Muscle-Trophic Factor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7, Word 5.1a
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RESULT 4  
US-08-726-817-1  
; Sequence 1, Application US/08726817  
; Patent No. 5707616  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June

Query Match:	100.0%	Score 489;	DB 1;	Length 489;
Best Local Similarity:	100.0%;	Pred. No. 1.6e-124;		
Matches 489;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

  

QY	1	ATGAGATTTCGAAACCATTTGGAGAGTATTTTCATCCAGTCTACTGTGTTACTT	60
Db	1	ATGAGATTTCGAAACCATTTGGAGAGTATTTTCATCCAGTCTACTGTGTTACTT	60
QY	61	CTAAACAGTCATTTCTACTGAACCTGGCATTCATGTCTTCAATTTGGCGCTGTTTCAGT	120
Db	61	CTAAACAGTCATTTCTACTGAACCTGGCATTCATGTCTTCAATTTGGCGCTGTTTCAGT	120
QY	121	GCAGGGCTTCCTAAACAGAACGCCAATCGGGGTAATGTAATAGTATTTGAAAAAATTT	180
Db	121	GCAGGGCTTCCTAAACAGAACGCCAATCGGGGTAATGTAATAGTATTTGAAAAAATTT	180
QY	181	GAGATCTTATTCATCTATGTCATTTATGCTTACTTTATATACGAAAGTGATGTTCCAC	240
Db	181	GAGATCTTATTCATCTATGTCATTTATGCTTACTTTATATACGAAAGTGATGTTCCAC	240
QY	241	CCCAAGTTCGAAGTAACAGCAATGAAGAGCTTCTCCTTGGAGTACAAAGTTATTTCACCT	300
Db	241	CCCAAGTTCGAAGTAACAGCAATGAAGAGCTTCTCCTTGGAGTACAAAGTTATTTCACCT	300
QY	301	GAGTCCGGAGATGCAAGTATTCATGATACAGTACAAAATCTGATCATCTAGCAAAACAC	360
Db	301	GAGTCCGGAGATGCAAGTATTCATGATACAGTACAAAATCTGATCATCTAGCAAAACAC	360
QY	361	AGTTTGTCTTCTTAAGGGAATGTAACAAATCTGGATGCAAAAGATGTGAGAACTGGAG	420
Db	361	AGTTTGTCTTCTTAAGGGAATGTAACAAATCTGGATGCAAAAGATGTGAGAACTGGAG	420



Best Local Similarity 100.0%; Pred. No. 1.6e-124;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAGATTTCGAACACATTTGAGAGATTTCCATCCAGTGTACTGTGTACTT 60
  |||
Db 1 ATGAGATTTCGAACACATTTGAGAGATTTCCATCCAGTGTACTGTGTACTT 60
QY 61 CTAAACAGTATTTTCTACTGAGTGTGATTCATGTCCTTCAATTTGGCTGTT 120
  |||
Db 61 CTAAACAGTATTTTCTACTGAGTGTGATTCATGTCCTTCAATTTGGCTGTT 120
QY 121 GCAGGCTTCCTTAAACAGAGCAACTGGTGAATGTAATAAGTATTTGAAAAAAT 180
  |||
Db 121 GCAGGCTTCCTTAAACAGAGCAACTGGTGAATGTAATAAGTATTTGAAAAAAT 180
QY 181 GAAGATCTTATTCATATTCATGATGATGATGATGATGATGATGATGATGAT 240
  |||
Db 181 GAAGATCTTATTCATATTCATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 CCAGTTGCAAAATGACAGAAATGAGTGTCTCTGAGTTACAGTTATTTCACT 300
  |||
Db 241 CCAGTTGCAAAATGACAGAAATGAGTGTCTCTGAGTTACAGTTATTTCACT 300
QY 301 GAGTCGGAGATGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 360
  |||
Db 301 GAGTCGGAGATGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 AGTTGCTCTTAATGGAATGTAACAGAAATGTAAGTGTGAGTGTGAGTGTGAG 420
  |||
Db 361 AGTTGCTCTTAATGGAATGTAACAGAAATGTAAGTGTGAGTGTGAGTGTGAG 420
QY 421 GAAAAAATATTAAGATTTTGGCAGATTTTGTACATATTTGTCCAAAATGTCATCA 480
  |||
Db 421 GAAAAAATATTAAGATTTTGGCAGATTTTGTACATATTTGTCCAAAATGTCATCA 480
QY 481 ACTTCTTGA 489
  |||
Db 481 ACTTCTTGA 489
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## RESULT 7

US-08-725-969-1  
Sequence 1, Application US/08725969  
Patent No. 5892001  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
City: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/725,969  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.

REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-08-725-969-1

Query Match 100.0%; Score 489; DB 2; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.6e-124;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAGATTTCGAACACATTTGAGAGATTTCCATCCAGTGTACTGTGTACTT 60
  |||
Db 1 ATGAGATTTCGAACACATTTGAGAGATTTCCATCCAGTGTACTGTGTACTT 60
QY 61 CTAAACAGTATTTTCTACTGAGTGTGATTCATGTCCTTCAATTTGGCTGTT 120
  |||
Db 61 CTAAACAGTATTTTCTACTGAGTGTGATTCATGTCCTTCAATTTGGCTGTT 120
QY 121 GCAGGCTTCCTTAAACAGAGCAACTGGTGAATGTAATAAGTATTTGAAAAAAT 180
  |||
Db 121 GCAGGCTTCCTTAAACAGAGCAACTGGTGAATGTAATAAGTATTTGAAAAAAT 180
QY 181 GAAGATCTTATTCATATTCATGATGATGATGATGATGATGATGATGATGAT 240
  |||
Db 181 GAAGATCTTATTCATATTCATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 CCAGTTGCAAAATGACAGAAATGAGTGTCTCTGAGTTACAGTTATTTCACT 300
  |||
Db 241 CCAGTTGCAAAATGACAGAAATGAGTGTCTCTGAGTTACAGTTATTTCACT 300
QY 301 GAGTCGGAGATGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 360
  |||
Db 301 GAGTCGGAGATGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 360
QY 361 AGTTGCTCTTAATGGAATGTAACAGAAATGTAAGTGTGAGTGTGAGTGTGAG 420
  |||
Db 361 AGTTGCTCTTAATGGAATGTAACAGAAATGTAAGTGTGAGTGTGAGTGTGAG 420
QY 421 GAAAAAATATTAAGATTTTGGCAGATTTTGTACATATTTGTCCAAAATGTCATCA 480
  |||
Db 421 GAAAAAATATTAAGATTTTGGCAGATTTTGTACATATTTGTCCAAAATGTCATCA 480
QY 481 ACTTCTTGA 489
  |||
Db 481 ACTTCTTGA 489
```

## RESULT 8

US-08-794-524-1  
Sequence 1, Application US/08794524  
Patent No. 5985262  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
City: Seattle

STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/794,524  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-08-794-524-1

Query Match 100.0%; Score 489; DB 2; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1,6e-124; Indels 0; Gaps 0;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTCCAAACCCACATTTGAGAGTATTTCCATCCAGTGTACTTGTGTTACTT 60  
DB 1 ATGAGATTTTCCAAACCCACATTTGAGAGTATTTCCATCCAGTGTACTTGTGTTACTT 60  
QY 61 CTAACAGATTTTCTTAACGAGCTGGATTCATGCTTCTTCAATTTGGGCTGTTCACT 120  
DB 61 CTAACAGATTTTCTTAACGAGCTGGATTCATGCTTCTTCAATTTGGGCTGTTCACT 120  
QY 121 GCAGGGCTTCTTAACGAGAGCCAACTGGGTGAATGTAATAGTATTTGAAAAAATT 180  
DB 121 GCAGGGCTTCTTAACGAGAGCCAACTGGGTGAATGTAATAGTATTTGAAAAAATT 180  
QY 181 GAAGATCTTATTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
DB 181 GAAGATCTTATTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
QY 241 CCCAGTTCGAAAGTAAACGAGATGAGTCTTCTTGGAGTTACAGTATTTTCACTT 300  
DB 241 CCCAGTTCGAAAGTAAACGAGATGAGTCTTCTTGGAGTTACAGTATTTTCACTT 300  
QY 301 GAGTCCGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTAGCAAAACAC 360  
DB 301 GAGTCCGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTAGCAAAACAC 360  
QY 361 AGTTGTTCTTAATGGGAGATGTAACAGATCTGATGATGATGATGATGATGATGATGAT 420  
DB 361 AGTTGTTCTTAATGGGAGATGTAACAGATCTGATGATGATGATGATGATGATGATGAT 420  
QY 421 GAAAAAATATTAAGATTTTTCAGAGTCTTGTACATATTTGCAAAATGTTATATCAC 480  
DB 421 GAAAAAATATTAAGATTTTTCAGAGTCTTGTACATATTTGCAAAATGTTATATCAC 480  
QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489

RESULT 9  
US-09-134-132-2  
Sequence 2, Application US/09134132  
Patent No. 6013480  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Paxton, Raymond  
TITLE OF INVENTION: Antagonists of IL-15  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,132  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,317  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-09-134-132-2

Query Match 100.0%; Score 489; DB 3; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1,6e-124; Indels 0; Gaps 0;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACCAACATTTGAGAGTATTTCCATCCAGTGTACTTGTGTTACTT 60  
DB 1 ATGAGATTTTGAACCAACATTTGAGAGTATTTCCATCCAGTGTACTTGTGTTACTT 60  
QY 61 CTAACAGATTTTCTTAACGAGCTGGATTCATGCTTCTTCAATTTGGGCTGTTCACT 120  
DB 61 CTAACAGATTTTCTTAACGAGCTGGATTCATGCTTCTTCAATTTGGGCTGTTCACT 120  
QY 121 GCAGGGCTTCTTAACGAGAGCCAACTGGGTGAATGTAATAGTATTTGAAAAAATT 180  
DB 121 GCAGGGCTTCTTAACGAGAGCCAACTGGGTGAATGTAATAGTATTTGAAAAAATT 180  
QY 181 GAAGATCTTATTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
DB 181 GAAGATCTTATTCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
QY 241 CCCAGTTCGAAAGTAAACGAGATGAGTCTTCTTGGAGTTACAGTATTTTCACTT 300  
DB 241 CCCAGTTCGAAAGTAAACGAGATGAGTCTTCTTGGAGTTACAGTATTTTCACTT 300



TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-09-134-456-2

Query Match 100.0%; Score 489; DB 4; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.6e-124;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGATTTCGAACACACATTGGAGATATTCATCCAGTGTCTACTTGTACTT 60  
1 ATGAGATTTCGAACACACATTGGAGATATTCATCCAGTGTCTACTTGTACTT 60  
61 CTAACAGCTTTTCTAATGATGATGATGATGATGATGATGATGATGATGAT 120  
61 CTAACAGCTTTTCTAATGATGATGATGATGATGATGATGATGATGATGAT 120  
121 GCAGGCTTCTTAACAGACCAAGTGGTGAATGTAATGATGATGATGATGAT 180  
121 GCAGGCTTCTTAACAGACCAAGTGGTGAATGTAATGATGATGATGATGAT 180  
181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGAT 240  
181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGAT 240  
241 CCCAGTTCGAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
241 CCCAGTTCGAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
301 GAGTCCGAGATGCAAGTATGATGATGATGATGATGATGATGATGATGATGAT 360  
301 GAGTCCGAGATGCAAGTATGATGATGATGATGATGATGATGATGATGATGAT 360  
361 AGTTGCTTTCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
361 AGTTGCTTTCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATTTGTCCTCAATGTCATC 480  
421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATTTGTCCTCAATGTCATC 480  
481 ACTTCTGA 489  
481 ACTTCTGA 489

RESULT 12  
US-09-196-427-2  
Sequence 2, Application US/09196427  
Patent No. 6177079  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Paxton, Raymond  
TITLE OF INVENTION: Antagonists of IL-15  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/196,427

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/392,317  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-09-196-427-2

Query Match 100.0%; Score 489; DB 4; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.6e-124;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGAGATTTCGAACACACATTGGAGATATTCATCCAGTGTCTACTTGTACTT 60  
1 ATGAGATTTCGAACACACATTGGAGATATTCATCCAGTGTCTACTTGTACTT 60  
61 CTAACAGCTTTTCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 120  
61 CTAACAGCTTTTCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 120  
121 GCAGGCTTCTTAACAGACCAAGTGGTGAATGTAATGATGATGATGATGATGAT 180  
121 GCAGGCTTCTTAACAGACCAAGTGGTGAATGTAATGATGATGATGATGATGAT 180  
181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
181 GAAGATCTTATTCATATGATGATGATGATGATGATGATGATGATGATGATGAT 240  
241 CCCAGTTCGAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
241 CCCAGTTCGAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 300  
301 GAGTCCGAGATGCAAGTATGATGATGATGATGATGATGATGATGATGATGAT 360  
301 GAGTCCGAGATGCAAGTATGATGATGATGATGATGATGATGATGATGATGAT 360  
361 AGTTGCTTTCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
361 AGTTGCTTTCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATTTGTCCTCAATGTCATC 480  
421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATTTGTCCTCAATGTCATC 480  
481 ACTTCTGA 489  
481 ACTTCTGA 489

RESULT 13  
US-09-189-193-1  
Sequence 1, Application US/09189193  
Patent No. 6184359  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June





Db	181	GAATATCTTAATTCATCATCATGATTTGATGTCACCTTATATATACGGAAGATGATTTCCAC	240
QY	241	CCGAGTTGCAGAAAGTAAACAGCAATGAAGTTCCTTCTTGAGATTACAAAGTATATTTCACTT	300
Db	241	CCCATTTGCAGAAAGTAAACAGCAATGAAGTTCCTTCTTGAGATTACAAAGTATATTTCACTT	300
QY	301	GAGTCGCGAGATGCAAGTATTTTCATGATATACAGTAGAAAAATCTGATCATCTTCAGCAAAACAC	360
Db	301	GAGTCGCGAGATGCAAGTATTTTCATGATATACAGTAGAAAAATCTGATCATCTTCAGCAAAACAC	360
QY	361	AGTTTGCTTCTATATGGAGATGTATACAGATCTTCGATGCAAGAAATGTAGGAACTTGAG	420
Db	361	AGTTTGCTTCTATATGGAGATGTATACAGATCTTCGATGCAAGAAATGTAGGAACTTGAG	420
QY	421	GAAGAAAAATATTTAAAGATTTTTCGCAGAGTTTGTATACATATTTGTCCAAAATGTTTCATCAAC	480
Db	421	GAAGAAAAATATTTAAAGATTTTTCGCAGAGTTTGTATACATATTTGTCCAAAATGTTTCATCAAC	480
QY	481	ACTTCTTGA	489
Db	481	ACTTCTTGA	489

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RESULT 15
PCT-US96-06423-1
: Sequence 1, Application PC/TUS9606423
: GENERAL INFORMATION:
: APPLICANT: Immunex Corporation
: TITLE OF INVENTION: Muscle Trophic Factor
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98101
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh
: OPERATING SYSTEM: System 7, Word 6.0
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION NUMBER:
: APPLICATION NUMBER: PC/TUS96/06423
: FILING DATE: 07 May 1996
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Malaska, Stephen L.
: REGISTRATION NUMBER: 32,655
: REFERENCE/DOCKET NUMBER: 2833-WO
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-587-0430
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 489 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..489
:
: PCT-US96-06423-1

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Query Match	100.0%;	Score 489;	DB 5;	Length 489;
Best Local Similarity	100.0%;	Pred. No. 1.6e-124;		
Matches 489;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 ATGAGAAATTTTGGAAACACACATTTGAGAAAGTATTTCCATCCAGTGTACTTGTGTTTACTT 600

Db 1 ATGAGAAATTTTGGAAACACACATTTGAGAAAGTATTTCCATCCAGTGTACTTGTGTTTACTT 600

OY	61	CTAAACGCTATTTTCTTAAGTGAAGCTGGCAATTCATGCTTTCATTTGGGCTGTTCCAGT	120
Db	61	CTAAACGCTATTTTCTTAAGTGAAGCTGGCAATTCATGCTTTCATTTGGGCTGTTCCAGT	120
OY	121	GCAGGGCTTCTTAAACGAGACCACATGGGTGAATGTAATAGTGAATTTGAAAAAAATT	180
Db	121	GCAGGGCTTCTTAAACGAGACCACATGGGTGAATGTAATAGTGAATTTGAAAAAAATT	180
OY	181	GAAATCTTATTCATCTATGTCATATTGATGCTACTTTATATACGGAAATGATGTTCCAC	240
Db	181	GAAATCTTATTCATCTATGTCATATTGATGCTACTTTATATACGGAAATGATGTTCCAC	240
OY	241	CCCAAGTTCGCAAGTACACGACATGAATGCTCTTCTCTTGAGGTACACAGTTATTTCCATT	300
Db	241	CCCAAGTTCGCAAGTACACGACATGAATGCTCTTCTCTTGAGGTACACAGTTATTTCCATT	300
OY	301	GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAANAATCGATCATCTGACCAAAACAC	360
Db	301	GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAANAATCGATCATCTGACCAAAACAC	360
OY	361	AGTTGTCTTCTAATGGGAATGTAAACGAATCTGGATGCAAAAGAAATGTGAGAACTGGAG	420
Db	361	AGTTGTCTTCTAATGGGAATGTAAACGAATCTGGATGCAAAAGAAATGTGAGAACTGGAG	420
OY	421	GAAAAAAATATTTAAAGAAATTTTTCGACAGTTTTGTACATATTGTCCAAATGTTTCATCCAC	480
Db	421	GAAAAAAATATTTAAAGAAATTTTTCGACAGTTTTGTACATATTGTCCAAATGTTTCATCCAC	480
OY	481	ACTTCTTGA 489	
Db	481	ACTTCTTGA 489	

Search completed: June 19, 2002, 00:51:46  
Job time: 4734 sec

Wed Jun 19 09:13:56 2002

us-09-724-841-1.rni

---



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:50:34 ; Search time 2237.54 Seconds  
(without alignments)  
2949.673 Million cell updates/sec

Title: US-09-724-841-4  
Perfect score: 489  
Sequence: 1 ATGAGAAATTCGAAACACACA.....TGTTCATCAACACTCTTGA 489

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estlov:\*  
5: em\_estlov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	95.1	982	9	AL548180
2	407.8	77.1	994	9	AL572832
3	377	73.1	509	9	AA463370
4	331.6	67.8	800	10	BG184658
5	276.6	56.6	637	9	AI860008
6	274.4	56.1	756	10	B1832895
7	236	48.3	872	10	B1758666
8	209	42.7	826	10	B1685668
9	165	33.7	690	9	AI596704
10	163.4	33.4	309	10	BF095213
11	161.2	31.0	471	10	N76741
12	151.6	31.0	515	10	BF704348
13	145.4	29.7	538	9	AI152482
14	145	29.7	564	9	AA863763
15	144.8	29.6	474	10	N49734
16	138	28.2	631	9	BB661271
17	126	25.8	166	10	BF379349

18	111.2	22.7	181	9	AA497102	AA497102	ae32d05.r
19	104.6	21.4	590	9	AA544986	AA544986	vk38h1.r
20	102.4	20.9	817	10	B1756810	B1756810	603024487
21	99.4	20.3	458	9	BB825167	BB825167	BB825167
22	98.4	20.1	430	9	AA838938	AA838938	UT-R-A0-a
23	96.6	19.8	420	10	BE690327	BE690327	uv66b02.y
24	86.8	17.8	548	9	BE698667	BE698667	RC2-UT002
25	84.6	17.3	648	9	AA874636	AA874636	vx81e08.r
26	84.4	17.3	429	9	AA863979	AA863979	vx87e05.r
27	82.8	16.9	718	10	B1766231	B1766231	603052877
28	81.8	16.7	434	9	AI503618	AI503618	vk38h12.x
29	80.4	16.4	494	9	AA804168	AA804168	PM4-UM008
30	74	15.1	405	9	AM121368	AM121368	UT-M-BH2
31	73.8	15.1	301	10	BF088290	BF088290	CM1-HT087
32	72.2	14.8	275	10	BF088272	BF088272	CM1-HT087
33	72.2	14.7	483	9	AA804165	AA804165	PM4-UM008
34	71.2	14.6	509	9	AI120615	AI120615	uc28h10.r
35	56.6	11.6	987	12	CNS014PQ	AL104456	Drosophila
36	54.2	11.1	278	9	BE177883	BE177883	RC3-HT060
37	52.8	10.8	391	12	A2334843	A2334843	1M064H21
38	52.8	9.6	1101	12	CNS000M2	AL063247	Drosophila
39	45.8	9.4	2017	11	BC004164	BC004164	Homo sapi
40	45.6	9.3	1101	12	CNS00396	AL063921	Drosophila
41	44.6	9.1	1204	12	CNS016E2	AL106628	Drosophila
42	44	9.0	540	10	B1814723	B1814723	PfEST0a0
43	44	9.0	584	10	B1815297	B1815297	PfEST0a1
44	43.2	8.8	740	10	BM167297	BM167297	EST565820
45	42.8	8.8	336	9	AM662994	AM662994	hn83h05.y

#### ALIGNMENTS

RESULT 1  
LOCUS AL548180 982 bp mRNA linear EST 16-FEB-2001  
DEFINITION AL548180 LTI.NFL006.PL2 Homo sapiens cDNA clone CS0D1034Y009 5  
prime, mRNA sequence.  
ACCESSION AL548180  
VERSION AL548180.1 GI:12882943  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 982)  
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

#### FEATURES

Location/Qualifiers  
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/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="CS0D1034Y009"

/clone\_id="LTI.NFL006.PL2"

/tissue="placenta"

/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA

was primed with a NotI-oligo(dt) primer. Five prime end

enriched, double-stranded cDNA was digested with NotI and

cloned into the NotI and EcoRV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by

Life Technologies. Contact: Feng Liang Life Technologies,

a division of Invitrogen 9800 Medical Center Drive

Rockville, Maryland 20850, USA Fax: (1) 301 610 8371

Email: fliang@life.com URL:

http://fulllength.invitrogen.com"

BASE COUNT 275 a 208 c 214 g 284 t

ORIGIN 1 others

Query Match 95.1%; Score 465; DB 9; Length 982;  
 Best Local Similarity 96.9%; Pred. No. 1.4e-93;  
 Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACACATTGAGAGATTTCCATCCAGCTGCTACCTGTTTACTT 60  
 Db ATGAGATTTCGAACACACATTGAGAGATTTCCATCCAGCTGCTACCTGTTTACTT 417  
 QY 61 CTAAGAGCTATTTCTTACGTAAGCTGCAATTCATCTTATTTGGGCTGTTTCACT 120  
 Db CTAAGAGCTATTTCTTACGTAAGCTGCAATTCATCTTATTTGGGCTGTTTCACT 477  
 QY 418 CTAAGAGCTATTTCTTACGTAAGCTGCAATTCATCTTATTTGGGCTGTTTCACT 477  
 Db CTAAGAGCTATTTCTTACGTAAGCTGCAATTCATCTTATTTGGGCTGTTTCACT 477  
 QY 121 GCAGGCTCCCTAAACAGAGCCAACTGGTGAATGTAATAGTATTGAAAAAAT 180  
 Db GCAGGCTCCCTAAACAGAGCCAACTGGTGAATGTAATAGTATTGAAAAAAT 537  
 QY 478 GCAGGCTCCCTAAACAGAGCCAACTGGTGAATGTAATAGTATTGAAAAAAT 537  
 Db GCAGGCTCCCTAAACAGAGCCAACTGGTGAATGTAATAGTATTGAAAAAAT 537  
 QY 181 GAAATCTTATTCATCTATGCAATTTGATGCTACTTATATACAGAAAGTATGTCAC 240  
 Db GAAATCTTATTCATCTATGCAATTTGATGCTACTTATATACAGAAAGTATGTCAC 597  
 QY 538 GAAATCTTATTCATCTATGCAATTTGATGCTACTTATATACAGAAAGTATGTCAC 597  
 Db GAAATCTTATTCATCTATGCAATTTGATGCTACTTATATACAGAAAGTATGTCAC 597  
 QY 241 CCCAGTTCAGAGTACAGCAATGAGTCTTCTGAGCTTGCAGCTTATTTTCACT 300  
 Db CCCAGTTCAGAGTACAGCAATGAGTCTTCTGAGCTTGCAGCTTATTTTCACT 657  
 QY 538 CCCAGTTCAGAGTACAGCAATGAGTCTTCTGAGCTTGCAGCTTATTTTCACT 657  
 Db CCCAGTTCAGAGTACAGCAATGAGTCTTCTGAGCTTGCAGCTTATTTTCACT 657  
 QY 301 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCCTACCAACAAC 360  
 Db GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCCTACCAACAAC 717  
 QY 658 GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCCTACCAACAAC 717  
 Db GAGTCCGAGATACAGATATTCATGATACAGTAAATCTTATCCTACCAACAAC 717  
 QY 361 ATCTGTTCTTATATGGAATATACAGATCTGATGCAAAAGTGTGAGACTAGAG 420  
 Db ATCTGTTCTTATATGGAATATACAGATCTGATGCAAAAGTGTGAGACTAGAG 777  
 QY 718 AGTTGTTCTTATATGGAATATACAGATCTGATGCAAAAGTGTGAGACTAGAG 777  
 Db AGTTGTTCTTATATGGAATATACAGATCTGATGCAAAAGTGTGAGACTAGAG 777  
 QY 421 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTTGCAATGTTCTATCAAC 480  
 Db GAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTTGCAATGTTCTATCAAC 837  
 QY 778 GAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTTGCAATGTTCTATCAAC 837  
 Db GAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTTGCAATGTTCTATCAAC 837  
 QY 481 ACTTCTTGA 489  
 Db ACTTCTTGA 846

RESULT 2  
 AL572832/c 994 bp mRNA linear EST 16-FEB-2001  
 LOCUS AL572832 LTI.NFL006.PL2 Homo sapiens cDNA clone CS0D1034Y009 3  
 DEFINITION prime, mRNA sequence.  
 ACCESSION AL572832  
 VERSION AL572832.1 GI:12931481  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 994)  
 AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.  
 FEATURES  
 source  
 1. .994  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CS0D1034Y009"  
 /clone\_lib="LTI.NFL006.PL2"  
 /tissue\_type="placenta"  
 /note="Vector: pCMVSPORT 6; site: 1; NotI; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-stranded cDNA was digested with Not I and  
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by  
 life Technologies. Contact : Feng Liang life Technologies,  
 a division of Invitrogen 9800 Medical Center Drive  
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
 Email : fliang@life.techn.com URL :  
 http://Fulllength.invitrogen.com"

BASE COUNT 333 a 186 c 154 g 316 t 5 others  
 ORIGIN

Query Match 83.4%; Score 407.8; DB 9; Length 994;  
 Best Local Similarity 95.4%; Pred. No. 7.5e-81;  
 Matches 415; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 55 TTACTCTTAAAGATCATTTTCTTAATGAAAGCTGGCATTCATGCTTCTCATTTGGGCTGT 114  
 Db TTACTCTTAAAGATCATTTTCTTAATGAAAGCTGGCATTCATGCTTCTCATTTGGGCTGT 935  
 QY 994 TTACTCTTAAAGATCATTTTCTTAATGAAAGCTGGCATTCATGCTTCTCATTTGGGCTGT 935  
 Db TTACTCTTAAAGATCATTTTCTTAATGAAAGCTGGCATTCATGCTTCTCATTTGGGCTGT 935  
 QY 115 TTCACTGAGGCTCCCTAAACAGAGCCAACTGGGTAATGTAATAGTATTTGAAA 174  
 Db TTCACTGAGGCTCCCTAAACAGAGCCAACTGGGTAATGTAATAGTATTTGAAA 875  
 QY 934 TTCACTGAGGCTCCCTAAACAGAGCCAACTGGGTAATGTAATAGTATTTGAAA 875  
 Db TTCACTGAGGCTCCCTAAACAGAGCCAACTGGGTAATGTAATAGTATTTGAAA 875  
 QY 175 AAAATGAAGATCTTATTCATCTATGCAATTTGATGCTACTTATATACAGAAAGTAT 234  
 Db AAAATGAAGATCTTATTCATCTATGCAATTTGATGCTACTTATATACAGAAAGTAT 815  
 QY 874 AAAATGAAGATCTTATTCATCTATGCAATTTGATGCTACTTATATACAGAAAGTAT 815  
 Db AAAATGAAGATCTTATTCATCTATGCAATTTGATGCTACTTATATACAGAAAGTAT 815  
 QY 235 GTTCAACCCAGTTGCAAGTACAGCAATGAGTCTTCTGAGTTCGCAAGTATTT 294  
 Db GTTCAACCCAGTTGCAAGTACAGCAATGAGTCTTCTGAGTTCGCAAGTATTT 755  
 QY 814 GTTCAACCCAGTTGCAAGTACAGCAATGAGTCTTCTGAGTTCGCAAGTATTT 755  
 Db GTTCAACCCAGTTGCAAGTACAGCAATGAGTCTTCTGAGTTCGCAAGTATTT 755  
 QY 295 TCACATGATTCGCGAGATACAGATATTCATGATACAGTAAATCTTATCCTTACGA 354  
 Db TCACATGATTCGCGAGATACAGATATTCATGATACAGTAAATCTTATCCTTACGA 695  
 QY 754 TCACATGATTCGCGAGATACAGATATTCATGATACAGTAAATCTTATCCTTACGA 695  
 Db TCACATGATTCGCGAGATACAGATATTCATGATACAGTAAATCTTATCCTTACGA 695  
 QY 355 AACACATCTTCTTCTTATGGAATATACAGATCTGATGCAAAAGTGTGAGAGAA 414  
 Db AACACATCTTCTTCTTATGGAATATACAGATCTGATGCAAAAGTGTGAGAGAA 635  
 QY 694 AACACATCTTCTTCTTATGGAATATACAGATCTGATGCAAAAGTGTGAGAGAA 635  
 Db AACACATCTTCTTCTTATGGAATATACAGATCTGATGCAAAAGTGTGAGAGAA 635  
 QY 415 CTGAGAGAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTTGCCAAAGTTC 474  
 Db CTGAGAGAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTTGCCAAAGTTC 575  
 QY 634 CTGAGAGAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTTGCCAAAGTTC 575  
 Db CTGAGAGAAAAAATATTAAGATTTTTCAGAGTTTGTACATATTTGCCAAAGTTC 575  
 QY 475 ATCAACACTTCTTGA 489  
 Db ATCAACACTTCTTGA 560

RESULT 3  
 AA463370 509 bp mRNA linear EST 10-JUN-1997  
 LOCUS zx97d12.r1 Soares.NHMPu.S1 Homo sapiens cDNA clone IMAGE:811703 5'  
 DEFINITION similar to SW-IL15\_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ;, mRNA  
 sequence.  
 ACCESSION AA463370  
 VERSION AA463370.1 GI:2188254  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 509)  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
 Kuwaba, T., Lacy, M., Le, N., Lennon, G., Merrin, M., Martin, J., Moore, B.,  
 Schellenberg, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wyllie,  
 T., Waterston, R. and Wilson, R.  
 TITLE WashU-Merck EST Project 1997  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium ([info@image.lnl.gov](mailto:info@image.lnl.gov)) for further information. Possible reversed clone: similarity on wrong strand. Seq primer: 28ml3 rev2. ET from Amersham. High quality sequence stop: 416.

## FEATURES

source

1..509

Location/Qualifiers

/organism="Homo sapiens"

/db\_xref="GDB:6042614"

/db\_xref="taxon:9606"

/clone="IMAGE:811703"

/clone\_lib="Soares\_NhMPu\_S1"

/tissue\_type="Pooled human melanocyte, fetal heart, and pregnant uterus"

/lab\_host="DH10B"

/note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site: 1: Not I; Site: 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDHM, pregnant uterus NBHPU, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT

149 a 91 c 108 g 161 t

ORIGIN

Query Match

77.1%; Score 377; DB 9; Length 509;

Best Local Similarity 96.3%; Pred. No. 5.3e-74;

Matches 366; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACCACTTTGAGAAGTATTTCCATCCAGTGCCTACTGTTTACTT 60  
 DB 105 ATGAGATTTCGAACCACTTTGAGAAGTATTTCCATCCAGTGCCTACTGTTTACTT 164  
 QY 61 CTAAAGATCATTTTCTAATGTAAGTGCATTCATCTTCAATTTGGGCTGTTTCACT 120  
 DB 165 CTAAAGATCATTTTCTAATGTAAGTGCATTCATCTTCAATTTGGGCTGTTTCACT 224  
 QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGTATTAAGTGAATTTGAAAAAATT 180  
 DB 225 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGTATTAAGTGAATTTGAAAAAATT 284  
 QY 181 GAAGATCTTATTCATCTATGATGATCTACTTATATACAGAAAGTATGTTTCACT 240  
 DB 285 GAAGATCTTATTCATCTATGATGATCTACTTATATACAGAAAGTATGTTTCACT 344  
 QY 241 CCCAGTTGCAAGGTACAGCAATGAGTCTTCTCTGGAAGTTCAGAAATTTTCACT 300  
 DB 345 CCCAGTTGCAAGGTACAGCAATGAGTCTTCTCTGGAAGTTCAGAAATTTTCACT 404  
 QY 301 GAGTCGGAGATACAGATATTCATGATACAGAAATCTTATACCTAGCAAAAC 360  
 DB 405 GAGTCGGAGATACAGATATTCATGATACAGAAATCTTATACCTAGCAAAAC 464  
 QY 361 ATCTTGCTCTTATGGAATATTAACAGAAATCTGATGCA 401  
 DB 465 AGTTTGCTCTTATGGAATATTAACAGAAATCTGATGCA 505

RESULT 4

LOCUS BG184658

DEFINITION RST3720 Atherys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BG184658

VERSION BG184658.1 GI:13706473

KEYWORDS EST.

SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

1 (bases 1 to 800)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,

Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J.,

Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith,

E., Veloso, N., Kilka, A., Hess, J., Cottrill, K., Lo, K., Offenbacher,

J., Danzig, J., and Ducar, M.

Creation of genome-wide protein expression libraries using random

activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

21227151

Contact: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: [scain@athersys.com](mailto:scain@athersys.com)

High quality sequence stop: 444.

Location/Qualifiers

1..800

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="Athersys RAGE Library"

/cell\_line="H1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is H1080, since a random activation method was used, these sequence tags are not necessarily expressed in H1080 under normal circumstances."

BASE COUNT

235 a 151 c 165 g 247 t

ORIGIN

Query Match

67.8%; Score 331.6; DB 10; Length 800;

Best Local Similarity 86.9%; Pred. No. 6.7e-64;

Matches 424; Conservative 0; Mismatches 54; Indels 10; Gaps 5;

QY 1 ATGGAATTTTGAACCACTTTGAGAAGTATTTCCATCCAGTGCCTACTGTTTACTT 60  
 DB 265 ATGGAATTTTGAACCACTTTGAGAAGTATTTCCATCCAGTGCCTACTGTTTACTT 324  
 QY 61 CTAAAGATCATTTTCTAATGTAAGTGCATTCATCTTCAATTTGGGCTGTTTCACT 120  
 DB 325 CTAAAGATCATTTTCTAATGTAAGTGCATTCATCTTCAATTTGGGCTGTTTCACT 384  
 QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGTATTAAGTGAATTTGAAAAAATT 180  
 DB 385 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGTATTAAGTGAATTTGAAAAAATT 444  
 QY 181 GAAGATCTTATTCATCTATGATGATCTACTTATATACAGAAAGTATGTTTCACT 240  
 DB 445 GAAGATCTTATTCATCTATGATGATCTACTTATATACAGAAAGTATGTTTCACT 504  
 QY 241 CCCAGTTGCAAGGTACAGCAATGAGTCTTCTCTGGAAGTTCAGAAATTTTCACT 300  
 DB 505 CCCAGTTGCAAGGTACAGCAATGAGTCTTCTCTGGAAGTTCAGAAATTTTCACT 564  
 QY 301 GAGTCGGAGATACAGATATTCATGATACAGAAATCTTATACCTAGCAAAAC 360  
 DB 565 GAGTCGGAGATACAGATATTCATGATACAGAAATCTTATACCTAGCAAAAC 622  
 QY 361 ATCTTGCTCTTATGGAATATTAACAGAAATCTGATGCA 420  
 DB 623 ATCTTGCTCTTATGGAATATTAACAGAAATCTGATGCA 480  
 QY 421 GAAAAAATTAAGATTTTTCAGAGTTTGTACATATTTGCCAATGTTTCAAC 480  
 DB 679 G-AAAAATTAAGATTTTTCAGAGTTTGTACATATTTGCCAATGTTTCAAC 734  
 QY 481 ACTTCTTG 488  
 DB 735 ACTTTTGG 742

clone distribution: NCICGWR clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: [www.bio.lnln.gov/bdbr/image/image.html](http://www.bio.lnln.gov/bdbr/image/image.html)  
Insert length: 3944 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 410.

Location/Qualifiers  
1. .637

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2436724"
/clone_1lb="NCI-GARP_U74"
/tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
/lab_host="DH10B"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"

```

BASE COUNT	207 a	111 c	91 g	227 t	1 others
ORIGIN					

Query Match	56.6%	Score 276.6	DB 9	Length 637
Best Local Similarity	95.0%	Pred. No. 1.1e-51		
Matches 285	Conservative 0	Mismatches 15	Indels 0	Gaps 0

QY	190	ATTCATCTTCATCATATGATGATGACTCTTTATATATCAGAAAGTATGTTCACCCAGTTGC	24.9
Db	637	ATTCATCTTCATCATATGATGATGACTCTTTATATATCAGAAAGTATGTTCACCCAGTTGC	57.8
QY	250	AAGTAAACAGCATGATGAAGTCTTCTCTTGAGCTTGCAGTATATTTACATGAGTCCGA	30.9
Db	577	AAATCTACACCAATGAAGTCTCTCTTGAGCTTGCAGTATATTTACATGAGTCCGA	51.8
QY	310	GATACAGATATTCATGATACAGTAAAGAAATCTTATCTATCTAGCAAAACATCTGTCT	36.9
Db	517	GATGCAAGTATTCATGATACAGTAAAGAAATCTGTATCTCTAGCAAAACATCTGTCT	45.8
QY	370	TCTATGCGAATATACAGATCTGCATGCAGAAAGTGTAGGAACTAGAGGAAAAAAT	42.9
Db	457	TCTATGCGAATATACAGATCTGCATGCAGAAAGTGTAGGAACTAGAGGAAAAAAT	39.8
QY	430	ATTAAAGAAATTTTGGCAGACTTTTGTATCATATATGTCCAAATGTTTCATCAACACTTCTTGA	48.9
Db	397	ATTAAAGAAATTTTGGCAGACTTTTGTATCATATATGTCCAAATGTTTCATCAACACTTCTTGA	35.8

Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Plate: LRAM1557 row: k column: 20  
 High quality sequence set: 756.

## FEATURES

Location/Qualifiers  
1. .756

**source**

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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:521771"
/clone_1ib="NIH_MGC_120"
/lab_host="DH10B"
/Note="Organ: pooled pancreas and spleen; Vector:
pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source: anonymous pool of spleen and pancreas from 28 yo
male. library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb. Insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

```

BASE COUNT	247 a	115 c	143 g	251 t
ORIGIN				

Query Match	56.1%	Score 274.4	DB 10	Length 756
Best Local Similarity	95.9%	Pred. No. 3	5e-51	
Matches 303	Conservative 0	Mismatches 11	Indels 2	Gaps 2

QY	174	AAAATTTGAAGATCTTTATTCACATCTATGCAATATTTGAATGACCTTATATATACAGAAAGTGA	233
Db	1	AAAATTTGAAGATCTTTATTCACATCTATGCAATATTTGAATGACCTTATATATACAGAAAGTGA	60
QY	234	TGTTACACCCAGTTGCAGGTAAACAGCAATGAAGTCTTCTCTGGAGTTGCAAGTTAT	233
Db	61	TGTTACACCCAGTTGCAGGTAAACAGCAATGAAGTCTTCTCTGGAGTTGCAAGTTAT	120
QY	294	TTTCACATGACATCCGGAGATTCAGATATTCATGATACAGTGAAGAAATCTTATTCATTCACAGC	353
Db	121	TTTCACATGACATCCGGAGATTCAGATATTCATGATACAGTGAAGAAATCTTATTCATTCACAGC	180
QY	354	AAACCAACATCTTGTCTCTAATGGGAATTAACAGAAATCGAGATCGCAAGAAATGTGAGGA	413
Db	181	AAACCAACCA - GTTGCTCTCTAATGGGAATTAACAGAAATCGAGATCGCAAGAAATGTGAGGA	239
QY	414	ACGAGAGGAAAAAATTTTAAAGAAATTTTGCAGAGTTTGTACATATGTGCCAAATGTT	473
Db	240	ACGAGAGGAAAAAATTTTAAAGAAATTTTGCAGAGTTTGTACATATGTGCCAAATGTT	298



QY 474 CATCACACTTCTTGA 489  
|||||  
Db 299 CATCACACTTCTTGA 314

RESULT 7  
BI758686 872 bp mRNA linear EST 25-SEP-2001  
LOCUS 603024240F1 NIH\_MGC\_114 Homo sapiens CDNA clone IMAGE:5194977 5',  
DEFINITION mRNA sequence.  
ACCESSION BI758686  
VERSION BI758686.1 GI:15750264  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 872)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: L14M11487 row: 0 column: 10  
High quality sequence start: 24  
High quality sequence stop: 859.

## FEATURES

## SOURCE

1. 872  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5194977"  
/clone\_1lib="NIH\_MGC\_114"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMV-Sport6; Site\_1: NotI;  
Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6  
male brains, age range 23-27 yo. Library is oligo-dT  
primed and directionally cloned (EcoRV site is destroyed  
upon cloning). Average insert size 1.5 kb, insert size  
range 1-3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 019. Note:  
this is a NIH\_MGC Library."

BASE COUNT 200 a 222 c 227 g 223 t  
ORIGIN

Query Match 48.3%; Score 236; DB 10; Length 872;  
Best Local Similarity 97.1%; Pred. No. 1.2e-42;  
Matches 272; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

QY 1 ATGAGATTGGAACCACTTTGGAAGTATTTCCATCCAGTGTACTGTTACTT 60  
|||||  
Db 592 ATGAGAAATTTGGAACCACTTTGGAAGTATTTCCATCCAGTGTACTGTTACTT 651  
QY 61 CTAAGAGCTATTTCTAAGCAAGCTGGCATTCATGCTTATTTGGGCTGTTCACT 120  
|||||  
Db 632 CTAAGAGCTATTTCTAAGCAAGCTGGCATTCATGCTTATTTGGGCTGTTCACT 711  
QY 121 GCAGGGCTCCCTAAACAGAACCCCACTGGGTGAATGTAATAGTATTGA-AAAAAT 179  
|||||  
Db 712 GCAGGGCTCCCTAAACAGAACCCCACTGGGTGAATGTAATAGTATTGA-AAAAAT 771  
QY 180 TGAAGATCTTATTCATCTATGCAATATGATGCTCTTATATACAGAAAGTATGTC 239  
|||||  
Db 772 TGAAGATCTTATTCATCTATGCAATATGATGCTCTTATATACAGAAAGTATGTC 831

QY 240 -CCCCAGTGCAGTAACA-GCAATGAAGTCTTCTCT 277  
|||||  
Db 832 CCCCCAGTGCAGTAACAAGCAATGAAGTCTTCTCT 871

RESULT 8  
BI685688 826 bp mRNA linear EST 18-SEP-2001  
LOCUS 60309529F1 NCI\_CGAP\_Mam6 Mus musculus CDNA clone IMAGE:5345382 5',  
DEFINITION mRNA sequence.  
ACCESSION BI685688  
VERSION BI685688.1 GI:15648316  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 826)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Jeffrey Green M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: L14M11877 row: j column: 07  
High quality sequence stop: 826.

## FEATURES

## SOURCE

1. 826  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5345382"  
/clone\_1lib="NCI CGAP Mam6"  
/sex="female, virgin"  
/tissue\_type="infiltrating ductal carcinoma"  
/dev\_stage="5 months"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-Sport6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 212 a 218 c 174 g 222 t  
ORIGIN

Query Match 42.7%; Score 209; DB 10; Length 826;  
Best Local Similarity 79.1%; Pred. No. 1.2e-36;  
Matches 273; Conservative 0; Mismatches 70; Indels 2; Gaps 2;

QY 1 ATGAGAAATTTGGAACCACTTTGGAAGTATTTCCATCCAGTGTACTGTTACTT 60  
|||||  
Db 481 ATGAGAAATTTGGAACCACTTTGGAAGTATTTCCATCCAGTGTACTGTTACTT 540  
QY 61 CTAAGAGCTATTTCTAAGCAAGCTGGCATTCATGCTTATTTGGGCTGTTCACT 120  
|||||  
Db 541 CTAAGAGCTATTTCTAAGCAAGCTGGCATTCATGCTTATTTGGGCTGTTCACT 599  
QY 121 GCAGGGCTCCCTAAACAGAACCCCACTGGGTGAATGTAATAGTATTGA-AAAAAT 180  
|||||  
Db 600 GTAGGCTCCCTAAACAGAACCCCACTGGGTGAATGTAATAGTATTGA-AAAAAT 659  
QY 181 GAAGATCTTATTCATCTATGCAATATGATGCTCTTATATACAGAAAGTATGTC 240  
|||||  
Db 660 GAAGATCTTATTCATCTATGCAATATGATGCTCTTATATACAGAAAGTATGTC 718  
QY 241 CCCAGTGCAGTAACAAGCAATGAAGTCTTCTCTTGGAGTGCAGTATTTCACAT 300  
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```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:948933"
/clone_lib="Soares_mammary_gland_NbMg"
/sex="male"
/tissue_type="mammary_gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5', TGTTGACCATCTGATGAGTGGAGCGGCGCGGAGATGTTTTTTTTTTTTTTTTTTTATCT3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. library constructed and normalized by Bento Soares and M.Patima Bonaldo."

```

Db 510 CTAACAGTCACCTTTTAACTGAGGCTGGCATTTCATGTCTTCATTNTGNGCTGTGICAGT 569

Qy	121	GCAGGCGTCCTTAACAGAACCCAACTGGGTGATGTAAATGAATTTGAAAAAATT	180
Db	570	GTAGGTCTCCCTTAACAGAGGCCAACTGGATAGATCTAAGATATGACCTGGAGAAAAATN	629
Qy	181	GAGATCTTAACTCATCTATGCGATATTGATGCTACTTTATATACAGAAATGA	233
Db	630	GAAAGCTTATTCATCTATTCATATTGACACCCACTMTATATACATGCACTGA	682

[illegible]

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 309)	Dias Neto, E., Garcia Correa, R., Veljovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsumura, A., Bala, G.S., Stimpson, D.H., Brumstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Stimpson, A.J.	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
2020263	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	
Contact:	Stimpson A.J.G.	

Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: [asimposon@ludwig.org.br](mailto:asimposon@ludwig.org.br)  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
project. This entry can be seen in the following URL:  
<http://www.ludwig.org.br/scr/scr/ps/gethtml2.pl?tl1=6t2-IL2-UT0071-050>  
900-144.B038t3-2000-09-03&cl=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 309.

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FEATURES
source
    Location/Qualifiers
        1..309
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_id="UT0071"
            /dev_stage="Adult"
            /note="Organ: uterus,tumor; Vector: puc18; Site:1: Sma1;
            Site:2: Sma1; A mini-library was made by cloning products
            derived from ORESTATS PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the pUC 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
BASE COUNT
110 a      48 c      55 g      96 t

```

	Query Match	33.4%	Score 163.4	DB 10,	Length 309;
	Best Local Similarity	93.98;	Pred. No. 1.7e-26;		
	Matches 170;	Conservative	0;	Mismatches 11;	Indels 0; Gaps 0;
OY	309 AGATGACAGATTTCATCATCAGTAGAAAACTTATCATCTGTACCAACAACATCTGTGC	368 			
Db	1 AGATGCCAGTTTCATCATATACAGTAGAAAATCTGATATCTGTACCAAAACAACATCTGTGC	60 			
OY	369 TTCTAATGGGAATTTAACAGCAATCTGATGCCAAAGAATGTGAGAACCTAGAGCGAAAAAAA	428 			
Db	61 TTCTAATGGGAATTTAATAGCATTTGGATGCCAAAGAATGTGAGAACCTGCGAGGAAAAAAA	120 			

61 TTCTAATGGGAATGTAATAGAATCTGGATGCAAGAATGTGAGGAACTGGAGGAAAAAA 120

[illegible]

## ORIGIN

Query Match 31.0%; Score 151.6; DB 10; Length 515;

Best Local Similarity 84.1%; Pred. No. 7.3e-24;

Matches 169; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

OY 289 GTTATTTTCACATGCTCGGAGATACAGATATTCATGATACAGAGAAAATCTTATCTC 348  
 DB 512 GTCAATTTTGCAAGAGCTCAGAAAATTCAGACATTTAGTACAGTAGAAAACCTTATCTC 453  
 OY 349 CTAGCAACACACATCTTCTCTCTATGGAATATACAGATCTGCAAGCAATGT 408  
 DB 452 CTTCGCAACAGAGTTTATGCTCATGTGATTAACGATGATCTGCAAGCAATGT 393  
 OY 409 GAGCACTAGAGCAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAA 468  
 DB 392 GAGGAGCTGAGCAAAAAATATTAACGATTTTGAAGAGTTTNTACATATCTGCCAA 333  
 OY 469 ATGTTTCATCACACTTCTTGA 489  
 DB 332 ATGTTTCATCACACTTCTTGA 312

RESULT 13  
 A1152482 538 bp mRNA linear EST 30-SEP-1998

LOCUS ud83d09.r1 Soares\_mammary\_gland\_NMLMG Mus musculus cDNA clone

DEFINITION IMAGE:1477457 5' similar to gb:U14332 Mus musculus Interleukin 15

(MOUSE); mRNA sequence.

ACCESSION A1152482 GI:3680951

VERSION EST.

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 538)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

CONTACT: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

MGI:925813

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 326.

Location/Qualifiers

1..538

/organism="Mus musculus"

/db\_xref="taxon:10090"

/clone\_1lb="Soares\_mammary\_gland\_NMLMG"

/sex="female (lactating)"

/tissue\_type="mammary gland"

/lab\_host="Dh10B"

/note="Vector: pRT73D-Pac (Pharmacia) with a modified

polylinker; 1st strand cDNA was prepared from mammary

gland tissue from a lactating female, and was then primed

with a Not I - oligo(dT) primer. Double-stranded cDNA was

ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the

modified pRT73 vector. Library is normalized. Library

BASE COUNT 163 a 108 c 103 g 163 t 1 others

was constructed by Bento Soares and M. Fatima Bonaldo.

## ORIGIN

Query Match 29.7%; Score 145.4; DB 9; Length 538;

Best Local Similarity 74.9%; Pred. No. 1.7e-22;

Matches 182; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

OY 247 TCGAAGTACAGCAAGAGAGTCTTCTCTGAGTTCGACGATTTATTCATGAGTCC 306  
 DB 532 TCGAAGTACAGCAAGAGAGTCTTCTCTGAGTTCGACGATTTATTCATGAGTCC 473  
 OY 307 GGAGTACAGATATTCATGATACAGTAAATCTTATTCATCTAGCAACACATCTTG 366  
 DB 472 AGTAACTGATCTTATTAAGAAACAGTAAAGCTGCTACCTTCAACAGCAGCTCG 413  
 OY 367 TCTTCTAAATGGGAATATACAGAAATCTGATGCAAGAAATGTGAGAACTAGAGAAA 426  
 DB 412 TCTTCTAAAGAAATGTAGCAAGAAATCTGCTGCAAGAAATGTGAGAACTAGAGAAA 353  
 OY 427 AATATTAAGATTTTTCGAGATTTGTACATATTTGCCAAATGTTTCATCACACTTCT 486  
 DB 352 ACCTTCACAGAGTTTTCGAAAGCTTTATACGATTTGCCAAATGTTTCATCACACTTC 293  
 OY 487 TGA 489  
 DB 292 TGA 290

RESULT 14

AA863763 564 bp mRNA linear EST 11-MAR-1998

LOCUS vx08d07.r1 Soares\_thymus\_2NBMt Mus musculus cDNA clone

DEFINITION IMAGE:1263853 5' similar to gb:U14332 Mus musculus Interleukin 15

(MOUSE); mRNA sequence.

ACCESSION AA863763 GI:2956242

VERSION EST.

KEYWORDS house mouse.

SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 564)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

CONTACT: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

MGI:666405

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 433.

Location/Qualifiers

1..564

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone\_1lb="Soares\_thymus\_2NBMt"

/sex="male"

/tissue\_type="thymus"

/dev\_stage="4 weeks"

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/organism="Homo sapiens"
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Search completed: June 19, 2002, 00:50:36  
Job time: 6344 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:51:46 Search time 60.38 Seconds  
(without alignments)  
1989.314 Million cell updates/second

Title:	US-09-724-841-4
Perfect score:	489
Sequence:	1 ATGAGAAATTGGAACCA.....TGTTATCAACACTTCTGA 489

Scoring table: IDENTITY\_NUC

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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1:  issued_patents_NA: *
2:  /cgn2_6/ptodata/2/1na/5A_COMB.seq: *
3:  /cgn2_6/ptodata/2/1na/5B_COMB.seq: *
4:  /cgn2_6/ptodata/2/1na/6A_COMB.seq: *
5:  /cgn2_6/ptodata/2/1na/5B_COMB.seq: *
6:  /cgn2_6/ptodata/2/1na/6CTUS_COMB.seq: *
7:  /cgn2_6/ptodata/2/1na/6ackfile1.seq: *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	489	100.0	489	1	US-08-031-399-1	Sequence 1, Appl
2	489	100.0	489	1	US-08-393-305-4	Sequence 4, Appl
3	489	100.0	489	1	US-08-726-817-4	Sequence 4, Appl
4	489	100.0	489	1	US-08-504-042-1	Sequence 1, Appl
5	489	100.0	489	1	US-08-352-117B-1	Sequence 1, Appl
6	489	100.0	489	2	US-08-725-669-4	Sequence 4, Appl
7	489	100.0	489	2	US-08-794-524-4	Sequence 4, Appl
8	489	100.0	489	3	US-09-134-132-1	Sequence 1, Appl
9	489	100.0	489	4	US-09-134-134A-1	Sequence 1, Appl
10	489	100.0	489	4	US-09-134-456-1	Sequence 1, Appl
11	489	100.0	489	4	US-09-196-827-1	Sequence 1, Appl
12	489	100.0	489	4	US-09-189-193-4	Sequence 4, Appl
13	100.0	489	5	PCT-US94-03793-1	Sequence 1, Appl	
14	465	95.1	489	1	US-08-031-399-4	Sequence 1, Appl
15	465	95.1	489	1	US-08-393-305-1	Sequence 1, Appl
16	465	95.1	489	1	US-08-535-733-1	Sequence 1, Appl
17	465	95.1	489	1	US-08-726-817-1	Sequence 1, Appl
18	465	95.1	489	1	US-08-504-042-4	Sequence 4, Appl
19	465	95.1	489	1	US-08-392-117B-2	Sequence 2, Appl
20	465	95.1	489	2	US-08-725-669-1	Sequence 1, Appl
21	465	95.1	489	2	US-08-794-524-1	Sequence 1, Appl
22	465	95.1	489	3	US-09-134-132-2	Sequence 2, Appl
23	465	95.1	489	4	US-09-134-134A-2	Sequence 2, Appl
24	465	95.1	489	4	US-09-134-456-2	Sequence 2, Appl
25	465	95.1	489	4	US-09-196-827-2	Sequence 2, Appl
26	465	95.1	489	4	US-09-189-193-1	Sequence 1, Appl
27	465	95.1	489	5	PCT-US94-03793-4	Sequence 4, Appl

28	465	95.1	489	5	PCT-US96-06433-1	Sequence 11, Appl1
29	465	95.1	1202	3	US-08-562-503-11	Sequence 11, Appl1
30	463.4	94.8	489	3	US-08-942-947-5	Sequence 5, Appl1
31	457	93.5	489	3	US-08-842-947-7	Sequence 7, Appl1
32	357.6	73.1	1248	2	US-09-000-141-1	Sequence 1, Appl1
33	345	70.6	345	1	US-08-993-305-13	Sequence 13, Appl1
34	345	70.6	345	1	US-08-726-817-13	Sequence 13, Appl1
35	345	70.6	345	2	US-08-726-817-13	Sequence 13, Appl1
36	345	70.6	345	2	US-08-794-524-13	Sequence 13, Appl1
37	345	70.6	345	4	US-08-193-193-13	Sequence 13, Appl1
38	325.8	66.6	345	4	US-08-189-131-12	Sequence 12, Appl1
39	325.8	66.6	345	1	US-08-93-305-12	Sequence 12, Appl1
40	325.8	66.6	345	2	US-08-726-817-12	Sequence 12, Appl1
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43	325.8	66.6	345	4	US-09-189-193-12	Sequence 12, Appl1
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45	36.6	7.5	3660	1	US-08-158-233-42	Sequence 42, Appl1
	36.6		3660	1	US-08-611-928-42	Sequence 42, Appl1

## ALIGNMENTS

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1
US-08-031-399-1
: Sequence 1, Application US/08031399
: Patent No. 5552303
:
: GENERAL INFORMATION:
: APPLICANT: Grabstein, Kenneth
: APPLICANT: Anderson, Dirk
: APPLICANT: Eisenman, June
: APPLICANT: Fung, Victor
: APPLICANT: Rauch, Charles
: TITLE OF INVENTION: Epithelium-derived T-cell Factor
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Immunex Corporation
: STREET: 51 University Street
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
:
: ZIP: 98101
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/031,399
: FILING DATE: 19930308
: CLASSIFICATION: 530
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Launet, Charlene
: REGISTRATION NUMBER: 33,035
: REFERENCE/DOCKET NUMBER: 2811
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 206-587-0430
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 489 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
:
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..489
:
: US-08-031-399-1

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Best Local Similarity 100.0%; Pred. No. 1,6e-123; Indels 0; Gaps 0;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGAGATTTCGAACACACATTGAGAAATATTCATCCAGTCTGCTGTTACTT 60  
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DB 121 GCAGGGCTCCCTAAACAGAACCACTGGTGAATGTAAATGATTTGAAAAATT 180  
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DB 361 ATCTTGCTCTTAATGGAATATTAACAGATCTGATGCAAAAGATGTAGAGACTAGAG 420  
QY 421 GAAAAAATATTAAGAAATTTTGCAGATTTTGTACATATTTGCCAAATGTTCAATCAAC 480  
DB 421 GAAAAAATATTAAGAAATTTTGCAGATTTTGTACATATTTGCCAAATGTTCAATCAAC 480  
QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489

RESULT 2  
US-08-393-305-4  
; Sequence 4, Application US/08393305  
; Patent No. 5574138  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/393,305  
; FILING DATE: 22-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 480052.409C2  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 489 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..489  
; US-08-393-305-4

Query Match 100.0%; Score 489; DB 1; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1,6e-123; Indels 0; Gaps 0;  
Matches 489; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGAGATTTCGAACACACATTGAGAAATATTCATCCAGTCTGCTGTTACTT 60  
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DB 61 CTAAGAGATCTTCTAATCTAATGAGTCTGCTGCTGCTGCTGCTGCTGCT 120  
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DB 421 GAAAAAATATTAAGAAATTTTGCAGATTTTGTACATATTTGCCAAATGTTCAATCAAC 480  
QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489

RESULT 3  
US-08-726-817-4  
; Sequence 4, Application US/08726817  
; Patent No. 5707616  
; GENERAL INFORMATION:  
; APPLICANT: Grabstein, Kenneth  
; APPLICANT: Anderson, Dirk  
; APPLICANT: Eisenman, June  
; APPLICANT: Fung, Victor  
; APPLICANT: Rauch, Charles  
; TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104



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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,817
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052,409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
; US-08-726-817-4
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Query Match          100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-123;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489
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RESULT 4  
US-08-504-042-1

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; Sequence 1, Application US/08504042
; Patent No. 5747024
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: Epithelium-derived T-cell Factor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/504,042
; FILING DATE: 19-JUL-1995
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/031,399
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Launer, Charlene
; REGISTRATION NUMBER: 33,035
; REFERENCE/DOCKET NUMBER: 2811
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
; US-08-504-042-1
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Query Match          100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-123;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 CCCAGTTGCAAGGTAAACAGCAATGAAGTCTTCTCTGAGTTGCAAGTTATTTACAT 300
DB 241 CCCAGTTGCAAGGTAAACAGCAATGAAGTCTTCTCTGAGTTGCAAGTTATTTACAT 300
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[illegible]

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US-08-392-317B-1
US-08-392-317B-1
Sequence 1, Application US/08392317B
Patent No. 5795966
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Paxton, Raymond
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Antagonists of IL-15
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Word for Windows 95, 7.0
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,317B
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..342
US-08-392-317B-1

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Query Match	100.0%;	Score 489;	DB 1;	length 489;
Best Local Similarity	100.0%;	Pred. NO. 1.6e-123;		
Matches 489;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db 1 ATGAGAAATTCGAACACACATTTGAGAGATATTCATCCAGTGTACTGTGTTACTT 600

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Db	121	GCAGGGGCTCCCTAAACAGAACGCCACTGGGTGAATGTAAATAGTGATTTGAAAAAAATTT	180
Oy	181	GAAAGTCTTATTCATCTATGCAATATGAGTCTCTTATATACAGAAAGTGAATGTTTCAC	240
Db	181	GAAAGTCTTATTCATCTATGCAATATGAGTCTCTTATATACAGAAAGTGAATGTTTCAC	240
Oy	241	CCCAAGTTCGAAGGTAAACAGCAATGAAGTGCCTTCTCTTGGAGTTGCAAGTATTTTCACAT	300
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RESULT 6  
 US-08-725-969-4  
 : Sequence 4, Application US/08725969  
 : Patent No. 5892001  
 : GENERAL INFORMATION:  
 : APPLICANT: Grabsteil, Kenneth  
 : APPLICANT: Anderson, Dirk  
 : APPLICANT: Elsemann, June  
 : APPLICANT: Fung, Victor  
 : APPLICANT: Rauch, Charles  
 : TITLE OF INVENTION: EPIHELUM-DERIVED T-CELL FACTOR  
 : NUMBER OF SEQUENCES: 15  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Seed and Berry  
 : STREET: 6300 Columbia Center, 701 Fifth Avenue  
 : CITY: Seattle  
 : STATE: Washington  
 : COUNTRY: USA  
 : ZIP: 98104  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/725,969  
 : FILING DATE: 04-OCT-1996  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/393,305  
 : FILING DATE: 22-FEB-1995  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Mcmasters, David D.  
 : REGISTRATION NUMBER: 33,963  
 : REFERENCE/DOCKET NUMBER: 480052.409C2  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 206-622-4900  
 : INFORMATION FOR SEQ. ID NO.: 4:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 489 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-08-725-969-4

Query Match 100.0%; Score 489; DB 2; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1,6e-123;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACACCAATTTGAGAAGTATTTCCATCCAGTGTCTACCTGTGTTACTT 60  
DB 1 ATGAGATTTTGAACACCAATTTGAGAAGTATTTCCATCCAGTGTCTACCTGTGTTACTT 60  
QY 61 CTAAGAGTCAATTTTCTAAGTGAAGCTGGCATTCATGCTTCTCATTTTGGCTGTTTCACT 120  
DB 61 CTAAGAGTCAATTTTCTAAGTGAAGCTGGCATTCATGCTTCTCATTTTGGCTGTTTCACT 120  
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QY 241 CCCAGTTGCAAGGTAAACGCAATGAGTCTTCTCTGGAGTTGCAAGTTATTTTCACT 300  
DB 241 CCCAGTTGCAAGGTAAACGCAATGAGTCTTCTCTGGAGTTGCAAGTTATTTTCACT 300  
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DB 481 ACTTCTTGA 489

RESULT 7  
US-08-794-524-4  
; Sequence 4, Application US/08794524  
; Patent No. 5985262  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/794,524  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-08-794-524-4

Query Match 100.0%; Score 489; DB 2; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1,6e-123;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACACCAATTTGAGAAGTATTTCCATCCAGTGTCTACCTGTGTTACTT 60  
DB 1 ATGAGATTTTGAACACCAATTTGAGAAGTATTTCCATCCAGTGTCTACCTGTGTTACTT 60  
QY 61 CTAAGAGTCAATTTTCTAAGTGAAGCTGGCATTCATGCTTCTCATTTTGGCTGTTTCACT 120  
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QY 181 GAAGATCTTATTCATATCATATGATGCTACTTTATATACAGAAAGTATGTTTCACT 240  
DB 181 GAAGATCTTATTCATATCATATGATGCTACTTTATATACAGAAAGTATGTTTCACT 240  
QY 241 CCCAGTTGCAAGGTAAACGCAATGAGTCTTCTCTGGAGTTGCAAGTTATTTTCACT 300  
DB 241 CCCAGTTGCAAGGTAAACGCAATGAGTCTTCTCTGGAGTTGCAAGTTATTTTCACT 300  
QY 301 GAGTCGGAGATACAGATATTCATGATACAGTAAATCTTATCATCTGCAAAACAC 360  
DB 301 GAGTCGGAGATACAGATATTCATGATACAGTAAATCTTATCATCTGCAAAACAC 360  
QY 361 ATCTGTCTTATGGAATATACAGATCTGATGCAAGAAATGTGAGAACTAGAG 420  
DB 361 ATCTGTCTTATGGAATATACAGATCTGATGCAAGAAATGTGAGAACTAGAG 420  
QY 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGCCAAATGTCATCAAC 480  
DB 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGCCAAATGTCATCAAC 480  
QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489

RESULT 8  
US-09-134-132-1  
; Sequence 1, Application US/09134132  
; Patent No. 6013480  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth

APPLICANT: Paxton, Raymond  
APPLICANT: Pettit, Dean  
TITLE OF INVENTION: Antagonists of IL-15  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,132  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,317  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..342  
US-09-134-132-1

Query Match 100.0%; Score 489; DB 3; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.6e-123;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACACATTTGAGAAATTTCCATCCAGTGCCTGTTACTT 60  
DB 1 ATGAGATTTCGAACACACATTTGAGAAATTTCCATCCAGTGCCTGTTACTT 60  
QY 61 CTTAAGAGTCATTTTCTAATCTGAGAGTGCATTCATGCTTCAATTTGGGCTGTTCACT 120  
DB 61 CTTAAGAGTCATTTTCTAATCTGAGAGTGCATTCATGCTTCAATTTGGGCTGTTCACT 120  
QY 121 GGAGGGCTCCCTAAACACAAAGCAACTGGGTGAATGTAATAGTATTTGAAAAAAT 180  
DB 121 GGAGGGCTCCCTAAACACAAAGCAACTGGGTGAATGTAATAGTATTTGAAAAAAT 180  
QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACAGAAAGTGATGTTAC 240  
DB 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTTATATACAGAAAGTGATGTTAC 240  
QY 241 CCCAGTTGCAAGGTACACAGCAATGAAGTCTTTCTCTGAGTTGCAAGTTATTTCAAT 300  
DB 241 CCCAGTTGCAAGGTACACAGCAATGAAGTCTTTCTCTGAGTTGCAAGTTATTTCAAT 300  
QY 301 GAGTCCGGAGATACAGATTTTCATGATACAGTAAATCTTATCTAGCAAAACAC 360  
DB 301 GAGTCCGGAGATACAGATTTTCATGATACAGTAAATCTTATCTAGCAAAACAC 360  
QY 361 ACTTGTCTTCTAATGGAATATACAGAAATCTGATGCAAGAAATGTAGCAACTAGAG 420

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DB 361 ACTTGTCTTCTAATGGAATATACAGAAATCTGATGCAAGAAATGTAGCAACTAGAG 420  
QY 421 GAAAAAATATTAAAGATTTTTCGACAGTTTGTACATATTGTCCAATGTTCAAC 480  
DB 421 GAAAAAATATTAAAGATTTTTCGACAGTTTGTACATATTGTCCAATGTTCAAC 480  
QY 481 ACTTGTGA 489  
DB 481 ACTTGTGA 489

RESULT 9  
US-09-134-134A-1  
Sequence 1, Application US/09134134A  
Patent No. 6165466  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Paxton, Raymond  
APPLICANT: Pettit, Dean  
TITLE OF INVENTION: Antagonists of IL-15  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,134A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/392,317  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..342  
US-09-134-134A-1

Query Match 100.0%; Score 489; DB 4; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.6e-123;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAACACACATTTGAGAAATTTCCATCCAGTGCCTGTTACTT 60  
DB 1 ATGAGATTTCGAACACACATTTGAGAAATTTCCATCCAGTGCCTGTTACTT 60  
QY 61 CTTAAGAGTCATTTTCTAATCTGAGAGTGCATTCATGCTTCAATTTGGGCTGTTCACT 120  
DB 61 CTTAAGAGTCATTTTCTAATCTGAGAGTGCATTCATGCTTCAATTTGGGCTGTTCACT 120

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1 RESULT 10
2 US-09-134-456-1
3 : Sequence 1, Application US/091344456
4 : Patent No. 6168783
5 : GENERAL INFORMATION:
6 : APPLICANT: Grabstein, Kenneth
7 : APPLICANT: Paxton, Raymond
8 : APPLICANT: Pettit, Dean
9 : TITLE OF INVENTION: Antagonists of IL-15
10 : NUMBER OF SEQUENCES: 10
11 : CORRESPONDENCE ADDRESS:
12 : ADDRESSEE: Immunex Corporation
13 : STREET: 51 University Street
14 : CITY: Seattle
15 : STATE: Washington
16 : COUNTRY: USA
17 : ZIP: 98101
18 : COMPUTER READABLE FORM:
19 : MEDIUM TYPE: Floppy disk
20 : COMPUTER: IBM PC Compatible
21 : OPERATING SYSTEM: Word for Windows 95, 7.0
22 : SOFTWARE: PatentIn Release #1.0, Version #1.25
23 : CURRENT APPLICATION DATA:
24 : APPLICATION NUMBER: US/09/134,456
25 : FILING DATE:
26 : CLASSIFICATION:
27 : PRIOR APPLICATION DATA:
28 : APPLICATION NUMBER: 08/392,317
29 : FILING DATE:
30 : ATTORNEY/AGENT INFORMATION:
31 : NAME: Malaska, Stephen L.
32 : REGISTRATION NUMBER: 32,655
33 : REFERENCE/DOCKET NUMBER: 2831
34 : TELECOMMUNICATION INFORMATION:
35 : TELEPHONE: 206-587-0430
36 : INFORMATION FOR SEQ ID NO: 1:
37 : SEQUENCE CHARACTERISTICS:
38 : LENGTH: 489 base pairs
39 : TYPE: nucleic acid
40 : STRANDEDNESS: single
41 : TOPOLOGY: linear
42 : MOLECULE TYPE: cDNA
43 : HYPOTHETICAL: NO

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Query Match      100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-123;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/392,317  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..342  
US-09-196-427-1

Query Match 100.0%; Score 489; DB 4; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.6e-123;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACACCATTTTGGAAGTATTTCCATCCAGTCTGCTGTTACTT 60  
DB 1 ATGAGATTTTGAACACCATTTTGGAAGTATTTCCATCCAGTCTGCTGTTACTT 60  
QY 61 CTAAGAGTCATTTTCTAATCTGATGATGCTGATTCATGCTTCTTCTTCTTCTT 120  
DB 61 CTAAGAGTCATTTTCTAATCTGATGATGCTGATTCATGCTTCTTCTTCTTCTT 120  
QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGTAATGATTTGAAAAAAT 180  
DB 121 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGTAATGATTTGAAAAAAT 180  
QY 181 GAAGATCTTATTCATCTATGATATGATGCTGATTCATTTATATACAGAAAGTATGTC 240  
DB 181 GAAGATCTTATTCATCTATGATATGATGCTGATTCATTTATATACAGAAAGTATGTC 240  
QY 241 CCCAGTTCAGAGTAACAGCAATGAAGTCTTCTCTTGAGCTTCAAGTTATTTCCAT 300  
DB 241 CCCAGTTCAGAGTAACAGCAATGAAGTCTTCTCTTGAGCTTCAAGTTATTTCCAT 300  
QY 301 GAGTCGGAGATACAGATATTCATGATACAGTAAATCTTATCATCTAGCAAAACAC 360  
DB 301 GAGTCGGAGATACAGATATTCATGATACAGTAAATCTTATCATCTAGCAAAACAC 360  
QY 361 ATCTGCTTCTAATGGAATATACAGAAATCTGATGCAAGATGTGAGAACTAGAG 420  
DB 361 ATCTGCTTCTAATGGAATATACAGAAATCTGATGCAAGATGTGAGAACTAGAG 420  
QY 421 GAAAAAATATTTAAGAAATTTTTCAGAGTTTGTACATATTTGCCAAATGTTCAATC 480  
DB 421 GAAAAAATATTTAAGAAATTTTTCAGAGTTTGTACATATTTGCCAAATGTTCAATC 480  
QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489

RESULT 12  
US-09-189-193-4  
Sequence 4, Application US/09189193  
Patent No. 6184359  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dlfk

APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/189,193  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-09-189-193-4

Query Match 100.0%; Score 489; DB 4; Length 489;  
Best Local Similarity 100.0%; Pred. No. 1.6e-123;  
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACACCATTTTGGAAGTATTTCCATCCAGTCTGCTGTTACTT 60  
DB 1 ATGAGATTTTGAACACCATTTTGGAAGTATTTCCATCCAGTCTGCTGTTACTT 60  
QY 61 CTAAGAGTCATTTTCTAATCTGATGATGCTGATTCATGCTTCTTCTTCTTCTT 120  
DB 61 CTAAGAGTCATTTTCTAATCTGATGATGCTGATTCATGCTTCTTCTTCTTCTT 120  
QY 121 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGTAATGATTTGAAAAAAT 180  
DB 121 GCAGGGCTCCCTAAACAGAACCACTGGGTGAATGTAATGATTTGAAAAAAT 180  
QY 181 GAAGATCTTATTCATCTATGATATGATGCTGATTCATTTATATACAGAAAGTATGTC 240  
DB 181 GAAGATCTTATTCATCTATGATATGATGCTGATTCATTTATATACAGAAAGTATGTC 240  
QY 241 CCCAGTTCAGAGTAACAGCAATGAAGTCTTCTCTTGAGCTTCAAGTTATTTCCAT 300  
DB 241 CCCAGTTCAGAGTAACAGCAATGAAGTCTTCTCTTGAGCTTCAAGTTATTTCCAT 300  
QY 301 GAGTCGGAGATACAGATATTCATGATACAGTAAATCTTATCATCTAGCAAAACAC 360  
DB 301 GAGTCGGAGATACAGATATTCATGATACAGTAAATCTTATCATCTAGCAAAACAC 360  
QY 361 ATCTGCTTCTAATGGAATATACAGAAATCTGATGCAAGATGTGAGAACTAGAG 420  
DB 361 ATCTGCTTCTAATGGAATATACAGAAATCTGATGCAAGATGTGAGAACTAGAG 420

Db 121 GCAGGCTCCCTAAACAGCAAGCCAACTGGGTGAATGTATTAAGTGATTTGAAAAAAATTT 180

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Query Match 95.1%; Score 465; DB 1; Length 489;  
Best Local Similarity 96.9%; Pred. No. 4.8e-117;  
Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 ATGGAATTTGAAACCACTTTGAGATTTTCCATCCAGTGTCTACTTACTT 60  
DB 1 ATGGAATTTGAAACCACTTTGAGATTTTCCATCCAGTGTCTACTTACTT 60  
QY 61 CTAAGAGCTATTTTCTTACTGAGCTGCAATTCATGCTTCAATTTGGGCTGTTTCACT 120  
DB 61 CTAAGAGCTATTTTCTTACTGAGCTGCAATTCATGCTTCAATTTGGGCTGTTTCACT 120  
QY 121 GCAGGGCTCCCTAAACGAAACCACTGGGTGAATGTAATAGTATTTGAAAAAAT 180  
DB 121 GCAGGGCTCCCTAAACGAAACCACTGGGTGAATGTAATAGTATTTGAAAAAAT 180  
QY 181 GAAGATCTTATTCATCTATGATTTGATGCTACTTATATACGAAAGATGTTTCACT 240  
DB 181 GAAGATCTTATTCATCTATGATTTGATGCTACTTATATACGAAAGATGTTTCACT 240  
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DB 241 CCCAGTTCCAGATACAGATATTCATGATACAGTAAATCTTATCCTTCAAGTTATTTTCACT 300  
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QY 481 ACTTCTTGA 489  
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RESULT 15  
US-08-393-305-1  
Sequence 1, Application US/08393305  
Patent No. 5574138  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
City: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/393,305  
FILING DATE: 22-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaisters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052,409C2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 489 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..489  
US-08-393-305-1

Query Match 95.1%; Score 465; DB 1; Length 489;  
Best Local Similarity 96.9%; Pred. No. 4.8e-117;  
Matches 474; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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DB 121 GCAGGGCTCCCTAAACGAAACCACTGGGTGAATGTAATAGTATTTGAAAAAAT 180  
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QY 481 ACTTCTTGA 489  
DB 481 ACTTCTTGA 489

Search completed: June 19, 2002, 00:51:47  
Job time: 4735 sec



Wed Jun 19 09:14:03 2002

us-09-724-841-4.rni

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:56:22 ; Search time 1924.67 Seconds  
(without alignments)  
195.710 Million cell updates/sec

Title: US-09-724-841-9  
Perfect score: 18  
Sequence: 1 AAYTGGGTNAAGTNAATH 18

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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1	14.4	80.0	18	6	AR004271	Sequence
2	14.4	80.0	18	6	AR070285	Sequence
3	14.4	80.0	18	6	AR085744	Sequence
4	14.4	80.0	18	6	I25786	Sequence 9
5	14.4	80.0	18	6	I28853	Sequence 9
6	14.4	80.0	18	6	I79223	Sequence 9
7	14.4	80.0	25	6	AR094646	Sequence
8	14.4	80.0	25	6	AR094646	Sequence
9	14.4	80.0	25	6	BD008808	Antagonists
10	14.4	80.0	39	6	AR024354	Sequence
11	14.4	80.0	39	6	AR122051	Sequence
12	14.4	80.0	39	6	AR122873	Sequence
13	14.4	80.0	39	6	AR125110	Sequence
14	14.4	80.0	69	6	AR024356	Sequence
15	14.4	80.0	69	6	AR122053	Sequence
16	14.4	80.0	69	6	AR122875	Sequence
17	14.4	80.0	69	6	AR125112	Sequence
18	14.4	80.0	345	6	AR070288	Sequence
19	14.4	80.0	345	6	AR070289	Sequence
20	14.4	80.0	345	6	AR085747	Sequence
21	14.4	80.0	345	6	AR085748	Sequence
22	14.4	80.0	345	6	I28856	Sequence 12
23	14.4	80.0	345	6	I28857	Sequence 12
24	14.4	80.0	345	6	I79226	Sequence 12
25	14.4	80.0	345	6	I79227	Sequence 13
26	14.4	80.0	380	11	G23879	human STRs
27	14.4	80.0	453	9	HS1L15MR	Sequence
28	14.4	80.0	484	5	AB067626	Sequence
29	14.4	80.0	486	6	HS1L15	Sequence
30	14.4	80.0	489	6	AR004267	Sequence
31	14.4	80.0	489	6	AR004268	Sequence
32	14.4	80.0	489	6	AR024348	Sequence
33	14.4	80.0	489	6	AR024349	Sequence
34	14.4	80.0	489	6	AR070281	Sequence
35	14.4	80.0	489	6	AR070282	Sequence
36	14.4	80.0	489	6	AR085740	Sequence
37	14.4	80.0	489	6	AR085741	Sequence
38	14.4	80.0	489	6	AR094649	Sequence
39	14.4	80.0	489	6	AR094650	Sequence
40	14.4	80.0	489	6	AR122045	Sequence
41	14.4	80.0	489	6	AR122046	Sequence
42	14.4	80.0	489	6	AR122867	Sequence
43	14.4	80.0	489	6	AR122868	Sequence
44	14.4	80.0	489	6	AR125104	Sequence
45	14.4	80.0	489	6	AR125105	Sequence

## ALIGNMENTS

RESULT 1	AR004271	18 bp	DNA	Linear	PAT 04-DEC-1998
LOCUS	AR004271	18 bp	DNA	Linear	PAT 04-DEC-1998
DEFINITION	Sequence 9 from patent US 5747024.				
ACCESSION	AR004271				
VERSION	AR004271.1	GI:3965150			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 18)				
AUTHORS	Grabstein,K.H. and Widmer,M.B.				
TITLE	Vaccine adjuvant comprising interleukin-15				
JOURNAL	Patent: US 5747024-A 9 05-MAY-1998;				
FEATURES	location/Qualifiers				
source	1..18				
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAYTGGTNAAYGTNATH 18  
Db 1 AAYTGGTNAAYGTNATH 18

RESULT 2  
AR070285  
LOCUS AR070285 18 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 9 from patent US 5892001.  
ACCESSION AR070285  
VERSION AR070285.1 GI:7221173  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Epithelium-derived T-cell factor antipodles  
JOURNAL Patent: US 5892001-A 9 06-APR-1999;  
FEATURES Location/Qualifiers  
source 1..18

BASE COUNT 5 a 0 c 4 g 4 t 5 others  
ORIGIN

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AR085744  
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DEFINITION Sequence 9 from patent US 5985262.  
ACCESSION AR085744  
VERSION AR085744.1 GI:10012510  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Method of treatment with epithelium derived T-cell factor  
JOURNAL Patent: US 5985262-A 9 16-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..18

BASE COUNT 5 a 0 c 4 g 4 t 5 others  
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RESULT 4  
I25786  
LOCUS I25786 18 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 9 from patent US 5552303.  
ACCESSION I25786  
VERSION I25786.1 GI:1605656

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Grabstein,K., Anderson,D., Eisenman,J., Fung,V. and Rauch,C.  
TITLE DNA encoding epithelium-derived T-cell factor  
JOURNAL Patent: US 5552303-A 9 03-SEP-1996;  
FEATURES Location/Qualifiers  
source 1..18

BASE COUNT 5 a 0 c 4 g 4 t 5 others  
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RESULT 5  
I28853  
LOCUS I28853 18 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 9 from patent US 5574138.  
ACCESSION I28853  
VERSION I28853.1 GI:1819635  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Epithelium-derived T-cell factor  
JOURNAL Patent: US 5574138-A 9 12-NOV-1996;  
FEATURES Location/Qualifiers  
source 1..18

BASE COUNT 5 a 0 c 4 g 4 t 5 others  
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Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
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RESULT 6  
I79223  
LOCUS I79223 18 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 9 from patent US 5707616.  
ACCESSION I79223  
VERSION I79223.1 GI:3207513  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Method for treating or preventing gastrointestinal disease with  
epithelium-derived T-cell factor  
JOURNAL Patent: US 5707616-A 9 13-JAN-1998;  
FEATURES Location/Qualifiers  
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BASE COUNT 5 a 0 c 4 g 4 t 5 others

## ORIGIN

## Query Match

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DB 1 AAYTGGTNAAYGTNATH 18

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LOCUS AR094646 25 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 1 from patent US 6001973.  
ACCESSION AR094646  
VERSION AR094646.1 GI:10021757  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Strom,T.B. and Maslinski,W.  
TITLE Antagonists of Interleukin-15  
JOURNAL Patent: US 6001973-A 1 14-DEC-1999;  
FEATURES  
source 1..25 Location/Qualifiers  
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Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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DB 8 AACTGGGTGAATGTATATA 25

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LOCUS AX320246 25 bp DNA linear PAT 14-DEC-2001  
DEFINITION Sequence 5 from Patent WO0187330.  
ACCESSION AX320246  
VERSION AX320246.1 GI:17901654  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (sites)  
AUTHORS Strom,T.B. and Maslinski,W.  
TITLE Compositions and methods for achieving immune suppression  
JOURNAL Patent: WO 0187330-A 5 22-NOV-2001;  
FEATURES  
source 1..25 Location/Qualifiers  
BASE COUNT 9 a 2 c 7 g 7 t  
ORIGIN

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Best Local Similarity 72.2%; Pred. No. 3.4e+02;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18  
DB 8 AACTGGGTGAATGTATATA 25

## RESULT 9

LOCUS BD008808 25 bp DNA linear PAT 31-JAN-2002  
DEFINITION Antagonists of Interleukin-15.  
ACCESSION BD008808  
VERSION BD008808.1 GI:18637181  
KEYWORDS JP 2001502521-A/1.  
SOURCE unidentified.  
ORGANISM unidentified.

## REFERENCE

1 (bases 1 to 25)  
AUTHORS Strom,T. and Maslinski,W.  
TITLE Antagonists of Interleukin-15  
JOURNAL Patent: JP 2001502521-A 1 27-FEB-2001;  
COMMENT BETH ISRAEL DEACONESS MEDICAL CENTER  
OS Unidentified  
PN JP 2001502521-A/1  
PD 27-FEB-2001  
PF 25-APR-1997 JP 1997539046  
PR 26-APR-1996 US 60/016634  
PI TERRY STROM,MLODZIMERZ MASLINSKI  
PC C12N15/24,C07K14/54,A61K38/20,C12N15/62,G01N33/68 CC  
CC Strandedness: Single;  
CC Topology: Linear;  
FH Key  
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Best Local Similarity 72.2%; Pred. No. 3.4e+02;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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DB 8 AACTGGGTGAATGTATATA 25

RESULT 10  
LOCUS AR024354 39 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 7 from patent US 5795966.  
ACCESSION AR024354  
VERSION AR024354.1 GI:3977648  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 39)  
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.  
TITLE Antagonists of Interleukin-15  
JOURNAL Patent: US 5795966-A 7 18-AUG-1998;  
FEATURES  
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BASE COUNT 12 a 8 c 9 g 10 t  
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Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Db 22 AACTGGGTGAATGTATA 39

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 DEFINITION Sequence 7 from patent US 6165466.  
 ACCESSION AR122051  
 VERSION AR122051.1 GI:14106368  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 39)  
 AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.  
 TITLE Antagonists of Interleukin-15  
 JOURNAL Patent: US 6165466-A 7 26-DEC-2000;  
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 Db 22 AACTGGGTGAATGTATA 39

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 AR122873  
 LOCUS AR122873 39 bp DNA Linear PAT 16-MAY-2001  
 DEFINITION Sequence 7 from patent US 6168783.  
 ACCESSION AR122873  
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 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 39)  
 AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.  
 TITLE Antagonists of Interleukin-15  
 JOURNAL Patent: US 6168783-A 7 02-JAN-2001;  
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 Db 22 AACTGGGTGAATGTATA 39

RESULT 13  
 AR125110  
 LOCUS AR125110 39 bp DNA Linear PAT 16-MAY-2001  
 DEFINITION Sequence 7 from patent US 6177079.  
 ACCESSION AR125110  
 VERSION AR125110.1 GI:14111172  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 39)  
 AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.  
 TITLE Antagonists of Interleukin-15  
 JOURNAL Patent: US 6177079-A 7 23-JAN-2001;  
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 LOCUS AR024356 69 bp DNA Linear PAT 05-DEC-1998  
 DEFINITION Sequence 9 from patent US 5795966.  
 ACCESSION AR024356  
 VERSION AR024356.1 GI:3977650  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 69)  
 AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.  
 TITLE Antagonists of Interleukin-15  
 JOURNAL Patent: US 5795966-A 9 18-AUG-1998;  
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RESULT 15  
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 DEFINITION Sequence 9 from patent US 6165466.  
 ACCESSION AR122053  
 VERSION AR122053.1 GI:14106370  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 69)  
 AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.  
 TITLE Antagonists of Interleukin-15  
 JOURNAL Patent: US 6165466-A 9 26-DEC-2000;  
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Wed Jun 19 09:14:04 2002

us-09-724-841-9.rge

Page 5

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Db 49 AACTGGGTGAATGTAATA 66

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:50:42 ; Search time 291.55 seconds  
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Title: US-09-724-841-9  
Perfect score: 18  
Sequence: 1 AAYTGCGTNAAYGTNATH 18

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Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
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Maximum Match 100%  
Listing first 45 summaries

Database :  
1: N\_Geneseq\_032802.\*  
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*  
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*  
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*  
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*  
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*  
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*  
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*  
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*  
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*  
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*  
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	80.0	18	AA00528	Degenerate PCR pri
2	14.4	80.0	18	AA084585	Simian IL-15 prime
3	14.4	80.0	18	AA049457	Epithelium derived
4	14.4	80.0	18	AA042244	Simian ERF gene pr
5	14.4	80.0	18	AAV02875	Simian epithelium
6	14.4	80.0	18	AA029483	Simian ERF DNA amp
7	14.4	80.0	18	AA238246	Simian ERF degen
8	14.4	80.0	22	AA057021	Simian ERF cDNA sp
9	14.4	80.0	25	AA097224	Mature Interleukin

10	14.4	80.0	39	AA036636	Interleukin-15 PCR
11	14.4	80.0	345	AA000525	Simian Interleukin
12	14.4	80.0	345	AA000527	Human Interleukin
13	14.4	80.0	345	AA057024	Simian ERF (SEF)
14	14.4	80.0	345	AA057025	Human ERF (SEF) m
15	14.4	80.0	466	AA021344	Human low adenosis
16	14.4	80.0	466	AA035222	Human adenosis re
17	14.4	80.0	466	AA00524	Simian Interleukin
18	14.4	80.0	466	AA00526	Human Interleukin
19	14.4	80.0	466	AA084583	Simian IL-15 clone
20	14.4	80.0	466	AA084584	Human IL-15 clone
21	14.4	80.0	466	AA049455	Simian epithelium
22	14.4	80.0	466	AA049456	Human epithelium d
23	14.4	80.0	466	AA042242	Simian epithelium
24	14.4	80.0	466	AA042243	Human epithelium
25	14.4	80.0	466	AA036634	Simian Interleukin
26	14.4	80.0	466	AA036635	Human Interleukin
27	14.4	80.0	466	AA097227	Wild-type Interleu
28	14.4	80.0	466	AA097228	Mutant Interleuk
29	14.4	80.0	466	AA058404	Interleukin-15 cod
30	14.4	80.0	466	AA023554	Human Interleukin
31	14.4	80.0	466	AA02874	Human Interleukin
32	14.4	80.0	466	AA02873	Simian epithelium
33	14.4	80.0	466	AA029479	Simian epithelium
34	14.4	80.0	466	AA029480	Human epithelium-d
35	14.4	80.0	466	AA090031	Simian Interleukin
36	14.4	80.0	466	AA090032	Human Interleukin
37	14.4	80.0	466	AA090033	Simian epithelium
38	14.4	80.0	466	AA038244	Human epithelium
39	14.4	80.0	466	AA038245	Human Interleukin
40	14.4	80.0	466	AA014465	Human Interleukin
41	14.4	80.0	466	AA057017	Simian ERF (SEF)
42	14.4	80.0	466	AA057018	Human ERF (SEF) p
43	14.4	80.0	565	AA035436	Human colon cancer
44	14.4	80.0	790	AA033078	Human IL-15 DNA
45	14.4	80.0	1202	AA056368	Human low adenosis
			21	AA021342	

## ALIGNMENTS

RESULT	1	
AA00528	AA00528 standard; cDNA; 18 BP.	
ID	AA00528:	
AC	AA00528:	
XX		
DT	02-FEB-1996 (first entry)	
XX		
DE	Degenerate PCR primer based on simian IL-15 mature N-terminus.	
XX		
KW	Interleukin-15; epithelium-derived T-cell factor; T lymphocyte;	
XX	PCR primer; ss.	
XX		
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	misc-feature	1..18
FT		/tag= a
FT		/note= "std IUPAC codes used"
PN	W09527722-A.	
PD	19-OCT-1995.	
XX		
XX	06-APR-1994;	94WO-US03793.
XX		
PR	06-APR-1994;	94WO-US03793.
XX		
PA	(IMMUNEX ) IMMUNEX CORP.	
XX		
XX	Anderson DM, Eisenman JR, Fung V, Grabstein KH;	
PI	Rauch C;	

XX WPI: 1995-373556/48.  
 DR Isolated DNA encoding polypeptide with mammalian IL-15 activity - which  
 XX stimulates proliferation and differentiation of T cells, used for  
 PT treating carcinoma(s), melanomas, etc. and viral infections  
 PT  
 XX Example; Page 21; 48pp; English.  
 PS  
 CC A simian species of IL-15 (sIL-15) was purified and analysed by SDS-  
 CC PAGE. Bioassay of unstained gel slices indicated IL-15 activity was  
 CC assoc. with proteins having mol. wts in the range of 15-17 kDa. The  
 CC N-terminus of the 15-17 kDa was sequenced. The results indicated the  
 CC identity of the first 33 AAs of AAR83309. Subsequent sequencing of a  
 CC cDNA clone obt'd. from a simian library provided a sequence encoding  
 CC the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA  
 CC leader sequence and a mature polypeptide AAR83309. The sequence of the  
 CC N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers  
 CC for the amplification of IL-15-specific DNA sequences. The first  
 CC 6 AAs of the N-terminus were used to design one primer, a  
 CC degenerate mixture coding for all possible codon usages - AAT00528.  
 CC The AA sequences of the simian mature N-terminus 26-31 were used  
 CC to design a second primer, a degenerate mixture coding for a  
 CC complement of all possible codon usages of AAs 26-31, omitting  
 CC postn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA  
 CC cells were used as templates. A 92 bp DNA fragment was used as a  
 CC hybridisation probe to screen a portion of a plasmid library contg.  
 CC cDNA inserts prep'd. from CV-1/EBNA polyadenylated RNA. This  
 CC resulted in the isolation of clone C85.sIL-15 that has an ORF  
 CC given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is  
 CC the precursor polypeptide.  
 SQ Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;

Query Match 80.0%; Score 14.4; DB 16; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAYTGCTNAAYGTNATH 18  
 |||  
 Db 1 aaytggynaaygtnath 18

## RESULT 2

AA084585  
 ID AA084585 standard; cDNA; 18 BP.

AC AA084585;

DT 04-SEP-1995 (first entry)

DE Simian IL-15 primer.

XX Interleukin-15; IL-15; sIL-15; T-cell growth factor;

KW African green monkey; CV-1; antitumor; virucide; primer; PCR;

KM polymerase chain reaction; ss.

XX Synthetic.

OS ZA9402636-A.

PN 28-DEC-1994.

PD 18-APR-1994; 94ZA-0002636.

PR 18-APR-1994; 94ZA-0002636.

XX (IMMV ) IMMUNEX CORP.

PA Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
 PI Rauch C;  
 XX

DR WPI: 1995-082473/11.  
 XX New purified interleukin-15 - which induces T cell proliferation  
 PT and differentiation, used for the treatment of tumours and viral  
 PT infection  
 PT  
 XX Example 3; Page 21; 47pp; English.  
 PS  
 CC cDNA generated from PMA-stimulated CV-1/EBNA cells was amplified  
 CC by PCR using primers (AA084585-87) based on the N-terminal sequence  
 CC of simian interleukin-15 (sIL-15). A clone encoding sIL-15 was  
 CC obtained (AA084583).  
 CC  
 SQ Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;

OY 1 AAYTGCTNAAYGTNATH 18  
 |||  
 Db 1 aaytggynaaygtnath 18

## RESULT 3

AA084585  
 ID AAT49457 standard; cDNA; 18 BP.

AC AAT49457;

DT 11-MAR-1997 (first entry)

DE Epithelium derived T cell factor PCR primer.

XX Simian epithelium derived T cell factor; sETF; African green monkey;

KW Cercopithecus aethiops; CV1/EBNA cell; T-cell; B-cell; lymphocyte;

KM proliferation; differentiation; gastrointestinal; HIV infection;

XX human immunodeficiency virus; polymerase chain reaction; ss.

OS Synthetic.

PN US5574138-A.

PD 12-NOV-1996.

PF 08-MAR-1993; 93US-0031399.

PR 22-FEB-1995; 95US-0393305.

PR 08-MAR-1993; 93US-0031399.

PR 22-APR-1994; 94US-0233606.

XX (IMMV ) IMMUNEX CORP.

PA Anderson DM, Eisenman JR, Fung V, Grabstein KH;

PI Rauch C;

DR WPI: 1996-517923/51.

XX New epithelium derived T cell factor - induces proliferation of T

PT and B cells, stimulates destruction of tumour and virus-infected

PT cells and protects against toxicity, partic. for treating intestinal

PT disease and HIV infection  
 PS Example 3; Column 25; 35pp; English.  
 CC The simian ETF (epithelium derived T cell factor) was isolated from  
 CC African green monkey CV1/EBNA cell conditioned medium. The N-  
 CC terminal sequence of the purified ETF was determined and then PCR  
 CC primers were designed based on the sequence information. The  
 CC present sequence is that of a degenerate primer based on the first 6  
 CC amino acids, i.e. Asn-Trp-Val-Asn-Val-Ile. A 92 bp fragment was  
 CC amplified from CV1/EBNA DNA and was used as a probe to screen a

CC CV1/EBNA CDNA library for the full-length SEF coding sequence.  
CC Mature SEF induces proliferation and/or differentiation of precursor  
CC or mature T cells and is useful for promoting long-term in vitro  
CC culture of T-lymphocytes and T-cell lines. It is used for treating  
CC gastrointestinal diseases including peptic ulcer, colitis and  
CC malignancy and for treating HIV infection.

XX Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;

Query Match 80.0%; Score 14.4; DB 17; Length 18;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAYTGGTNAAYGTNATH 18

Db 1 aaytg99gtnaaygtnath 18

RESULT 4

ID AAT42244

AAAT42244 standard; DNA; 18 BP.

AC AAT42244;

DT 05-FEB-1997 (first entry)

DE Simian ERF gene primer based on the 6 N-terminal amino acids.

KW Epithelium-derived T-cell factor; simian; human; culture; proliferation;

KW epithelial cell; differentiation; T-lymphocyte; African green monkey;

KW primer; PCR; polymerase chain reaction; amplification; probe; ss.

OS Synthetic.

PN USS552303-A.

PD 03-SEP-1996.

PF 08-MAR-1993; 93US-0031399.

PR 08-MAR-1993; 93US-0031399.

PA (IMMV ) IMMUNEX CORP.

PI Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;

DR WPI: 1996-412063/41.

PT New isolated simian and human epithelium-derived T-cell factors -

PT which stimulate the proliferation and/or differentiation of

PT T-lymphocytes and T-cell lines

PS Example 3; Column 17; 22pp; English.

CC Primers AAT42244-6 were used to amplify a 92 bp fragment of the African

CC green monkey epithelium-derived T-cell factor (ERF; AAT42243). The

CC sequence of this primer is based on the 6 N-terminal amino acids sequence

CC obtained by peptide sequencing the purified protein. The template for

CC the amplification was cDNA derived from monkey kidney CV-1/EBNA cells

CC stimulated to proliferate by phorbol 12-myristate 13-acetate. The 92 bp

CC fragment was labelled and used as a probe to isolate a clone C85. SEF

CC which contained the simian gene. ERF is a protein of 15-17 kD which is

CC expressed by epithelial cells and stimulates proliferation and/or

CC differentiation of precursor and/or mature T cells. The protein is

CC therefore useful for promoting long term in vivo culture of

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 AAYTGGTNAAYGTNATH 18  
Db 1 aaytg99gtnaaygtnath 18

RESULT 5

ID AAV02875

AAV02875 standard; DNA; 18 BP.

AC AAV02875;

DT 08-MAY-1998 (first entry)

DE Simian epithelium derived T-cell factor PCR primer 1.

KW Epithelium derived T-cell factor; ERF; simian; gastrointestinal disease;

KW B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;

KW treatment; prevention; PCR primer; ss.

OS Synthetic.

PN USS707616-A.

PD 13-JAN-1998.

PF 04-OCT-1996; 96US-0726817.

PR 22-FEB-1995; 95US-0393305.

PR 08-MAR-1993; 93US-0031399.

PR 22-APR-1994; 94US-0233606.

PA (IMMV ) IMMUNEX CORP.

PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;

DR WPI: 1998-100295/09.

PT Treatment or prevention of gastrointestinal diseases - by

PT administering epithelium-derived T-cell factor polypeptide

PS Example 3; Column 41-42; 34pp; English.

CC PCR primers AAV02875-V02877 are used in the amplification of a simian

CC epithelium-derived T-cell factor (ERF) which is used in a method for

CC treating or preventing gastrointestinal disease. These polypeptides have

CC particular application in the treatment of gastrointestinal disorders

CC associated with disruption of the gastrointestinal epithelium or villi

CC such as chemotherapy- and radiation-therapy induced enteritis (gut

CC toxicity), mucositis, peptic ulcer disease, gastroenteritis and colitis,

CC villus atrophic disorders, malignancy and inflammatory bowel disease.

CC ERF polypeptides may also be useful in the treatment of human

CC immunodeficiency virus (HIV) and HIV-associated disease due to their

CC ability to stimulate CD4+ and CD8+ cells. Biologically active ERF may be

CC used to treat a variety of other diseases or conditions where T-cell or

CC B-cell stimulation is desired.

XX Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;

Query Match 80.0%; Score 14.4; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAYTGGTNAAYGTNATH 18

Db 1 aaytg99gtnaaygtnath 18

RESULT 6

AAZ29483  
 ID AAZ29483 standard: DNA; 18 BP.  
 AC AAZ29483;  
 XX  
 XX  
 DT 10-JUN-1999 (first entry)  
 DE  
 XX  
 XX  
 DE Simlan ETF DNA amplifying primer.  
 XX  
 XX  
 KM Epithelium-derived T-cell factor; ETF; immunoassay; enteritis; ulcer;  
 KM T cell proliferation; gastrointestinal disease; mucositis; colitis;  
 KM gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease;  
 KM human immune deficiency virus; tumour; simlan; PCR primer; ss.  
 XX  
 XX  
 OS Synthetic.  
 OS  
 PN US5892001-A.  
 PN  
 XX  
 PD 06-APR-1999.  
 PD  
 XX  
 PF 04-OCT-1996; 96US-0725969.  
 PF  
 XX  
 PR 22-FEB-1995; 95US-0393305.  
 PR 08-MAR-1993; 93US-0031399.  
 PR 22-APR-1994; 94US-0233606.  
 PR 04-OCT-1996; 96US-0725969.  
 PR  
 XX  
 PA (IMV ) IMMUNEX CORP.  
 XX  
 XX  
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
 PI Rauch C;  
 PI  
 DR WPI: 1999-253930/21.  
 DR  
 XX  
 XX  
 PT Antibodies specific for epithelium-derived T-cell growth factor  
 PS  
 PS  
 XX  
 XX  
 PS Example 3; Columns 25; 34pp: English.  
 CC The invention relates to an isolated antibody that binds specifically to  
 CC a simlan or human epithelium-derived T-cell factor (ETF) polypeptide.  
 CC The antibodies are used, optionally when immobilized or labeled, to  
 CC detect and quantify ETF in standard immunoassays. They may also be used  
 CC as diagnostic and therapeutic agents, e.g. when conjugated to toxins (or  
 CC their precursors) or radionuclides. ETF induces proliferation and/or  
 CC differentiation of T cells (or their precursors), e.g. for use in  
 CC establishing long term in vitro cultures; and is also used to treat  
 CC gastrointestinal disease (e.g. enteritis or mucositis induced by  
 CC chemotherapy or radiation, peptic ulcer, gastroenteritis, colitis,  
 CC villus atrophy, malignancy and inflammatory bowel disease), to treat  
 CC human immune deficiency virus infection or associated disease, or  
 CC generally in any situation requiring stimulation of T or B cell  
 CC proliferation, secretion of immunoglobulins or certain cytokines,  
 CC increased anti-infectious disease immunity, induction of T-cell lytic  
 CC activity or increased destruction of tumour or virus-infected cells.  
 CC Sequences AAZ29483-85 represent primers for PCR amplification of the  
 CC simlan ETF DNA sequences.  
 CC  
 XX  
 XX  
 SQ Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;

Query Match 80.0%; Score 14.4; DB 20; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGCTNAAYCTNATH 18  
 ||||||||||||||||  
 Db 1 aaytgggtnaaygtnath 18

RESULT 7  
 AAZ38246  
 ID AAZ38246 standard: DNA; 18 BP.  
 XX

AAZ38246;  
 AC  
 XX  
 DT 09-FEB-2000 (first entry)  
 DE  
 XX  
 XX  
 DE Simlan ETF degenerate PCR primer #9.  
 KM  
 KM  
 KM ETF; epithelium-derived T-cell factor; T-cell; T-lymphocyte;  
 KM proliferation; differentiation; growth factor; precursor; mature; CD4+;  
 KM CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;  
 KM gastrointestinal disease; gastroenteritis; colitis;  
 KM inflammatory bowel disease; villus atrophic disorder; enteritis;  
 KM chemotherapy; radiotherapy; gut toxicity; cancer; side effect;  
 KM tolerated dose; PCR; primer; ss.  
 XX  
 XX  
 OS Synthetic.  
 OS  
 PN Mammalia.  
 PN  
 XX  
 PD US5985262-A.  
 PD  
 XX  
 PD 16-NOV-1999.  
 PD  
 XX  
 PF 03-FEB-1997; 97US-0794524.  
 PF  
 XX  
 PR 22-FEB-1995; 95US-0393305.  
 PR 04-OCT-1996; 96US-0726817.  
 PR 08-MAR-1993; 93US-0031399.  
 PR 22-APR-1994; 94US-0233606.  
 PR  
 XX  
 PA (IMV ) IMMUNEX CORP.  
 XX  
 XX  
 PI Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;  
 PI P-PSDB: AAZ52312.  
 PI  
 DR WPI: 2000-022267/02.  
 DR P-PSDB: AAZ52312.  
 DR  
 XX  
 XX  
 PT Stimulation of T-cells in human immunodeficiency virus infected  
 PT patients -  
 PS  
 PS  
 XX  
 XX  
 PS Example 3; Column 25; 33pp: English.  
 CC This sequence represents simlan ETF degenerate PCR primer #9, used with  
 CC degenerate primers #10 or #11 (AAZ38247, AAZ38248) to amplify a fragment  
 CC of the gene encoding simlan epithelium-derived T-cell factor (ETF).  
 CC This was used to probe a simlan cDNA library for a clone with a  
 CC complete open reading frame (AAZ38224). The primers were based on  
 CC N-terminal amino acid sequences in the purified ETF protein.  
 CC ETF is a previously unidentified T-cell growth factor which  
 CC stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to  
 CC proliferate and differentiate. It also promotes proliferation of the  
 CC gastrointestinal epithelium. The protein can be used to promote long-term  
 CC in vitro culture of T-lymphocytes and T-cell lines. ETF can be used for  
 CC treating HIV infection, HIV-associated diseases, and other diseases or  
 CC conditions where stimulation of T-cell proliferation would be desirable  
 CC e.g., it could be used to augment the destruction of tumour cells or  
 CC virally-infected cells. ETF may also be used to treat or prevent  
 CC gastrointestinal disease, including chemotherapy and radiotherapy  
 CC associated enteritis, gastroenteritis, colitis, inflammatory bowel  
 CC disease and villus atrophic disorders. Chemotherapy and radiotherapy  
 CC associated enteritis (gut toxicity) results in bleeding and sepsis due to  
 CC gastrointestinal flora entering the blood, and thus can limit the dosage  
 CC of therapeutic agent administered to a cancer patient. ETF may therefore  
 CC be used to increase the tolerated doses radiotherapy and chemotherapy.  
 CC  
 XX  
 XX  
 SQ Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;

Query Match 80.0%; Score 14.4; DB 21; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGCTNAAYCTNATH 18  
 ||||||||||||||||  
 Db 1 aaytgggtnaaygtnath 18

```

RESULT      8
ID AAF57021
XX AAF57021 standard; DNA: 18 BP.
AC AAF57021:
XX
XX 14-MAY-2001 (first entry)
DE Simian ETF cDNA specific degenerate primer.
XX
XX Epithelium-derived T-cell factor; ETF; simian; human; enteritis;
KM gastrointestinal disease; mucositis; peptic ulcer; cytostatic;
KM villus atrophic disorder; inflammatory bowel disease; antinflammatory;
XX anti-HIV; antiviral; T-lymphocyte stimulator; PCR primer; ss.
XX
XX Synthetic.
XX
XX US6184359-B1.
XX
XX 06-FEB-2001.
XX
XX 09-NOV-1998; 98US-0189193.
XX
XX 22-FEB-1995; 95US-0393305.
PR 04-OCT-1996; 96US-0725969.
PR 08-MAR-1993; 93US-0031399.
PR 22-APR-1994; 94US-0233606.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;
XX
XX WPI: 2001-217801/22.
XX
XX New antibodies that specifically binds epithelium-derived T-cell factor
PT polypeptide useful for e.g. treating or preventing gastrointestinal
PT diseases, HIV and HIV-associated diseases, augmenting destruction of
PT tumour cells -
XX
XX Example 3; Column 25; 35pp; English.
XX
XX The invention relates to simian and human epithelium-derived T-cell
XX factor (ETF) polypeptides. Antibodies that specifically bind to the ETF
XX polypeptides are used for treating or preventing gastrointestinal
XX diseases, such as chemotherapy and radiation therapy-induced enteritis
XX and mucositis, peptic ulcer disease, villus atrophic disorders and
XX inflammatory bowel disease; for increasing tolerated doses for radiation
XX therapy and chemotherapy agents which are limited by gastrointestinal
XX toxicity; and for treating HIV and HIV-associated diseases. The
XX conditions where it is desired to stimulate proliferation of
XX T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B
XX lymphocytes, to augment anti-infectious disease immunity, to induce CTL,
XX LAK or NK lytic activity, or to augment the destruction of tumour cells,
XX or cells infected with virus. Sequences AAF57021-23 represent PCR primers
XX used for simian ETF (sETF) cDNA cloning.
XX
XX Sequence 18 BP; 5 A; 0 C; 4 G; 4 T; 5 other;
XX
Query Match      80.0%; Score 14.4; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAYTGGGTNAAGTGNATH 18
   |||:|||||:|||||:|
Db 1 aaytgggtnaaagtgnath 18

```

RESULT 9  
AAT97224

```

ID AAT97224 standard; DNA: 25 BP.
XX
XX AAT97224:
AC AAT97224:
XX
XX 07-MAY-1998 (first entry)
DE Mature interleukin-15 (IL-15) cDNA amplifying primer 1.
XX
XX Interleukin-15; IL-15; mutant; human; treatment; autoimmune disease;
KM psoriasis; multiple sclerosis; rheumatic arthritis; immune response;
KM type 1 diabetes; AIDS; PCR primer; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX W09741232-A1.
XX
XX 06-NOV-1997.
XX
XX 25-APR-1997; 97WO-US06931.
XX
XX 26-APR-1996; 96US-0016634.
XX
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
XX Maslinski W, Strom T;
XX
XX WPI: 1997-549734/50.
XX
XX Mutant interleukin 15 polypeptide(s) - used for treating auto-immune
PT diseases e.g psoriasis, multiple sclerosis etc.
XX
XX Disclosure; Page 30; 86pp; English.
XX
XX This primer is used for the PCR amplification of the cDNA encoding a
XX mature interleukin-15 (IL-15) polypeptide. This is used in the
XX construction of a fusion protein FLAG-HM-IL-15. This fusion protein is
XX tested to determine whether it can interact with cell surface IL-15
XX receptors. A mutant IL-15 can be created by mutating the wild-type IL-15
XX at codon positions 149 and 156. The mutant polypeptide is at least 90%
XX identical to wild-type IL-15 and is capable of inhibiting at least one
XX of the cellular events that normally occurs when wild-type IL-15
XX specifically binds to a cell surface receptor. The mutant IL-15 is used
XX for suppressing the immune response in a patient. It can be used for
XX treating autoimmune diseases such as rheumatic arthritis, type I diabetes
XX or a rheumatic disease selected from systemic lupus erythematosus (SLE),
XX Sjogren's syndrome, scleroderma, mixed connective tissue disease,
XX dermatomyositis, polymyositis, Reiter's syndrome and Behcet's disease.
XX It can also be used to treat Hashimoto's thyroiditis, Grave's disease,
XX multiple sclerosis, myasthenia gravis, encephalomyelitis, a variety of
XX pemphigus, psoriasis, inflammatory bowel disease, AIDS and vascular
XX injury. The mutant IL-15 can also be used for reducing the viability of
XX a cell that expresses a IL-15 receptor. It can also be used to diagnose
XX a disease treatable with an IL-15 antagonist.
XX
XX Sequence 25 BP; 9 A; 2 C; 7 G; 7 T; 0 other;
XX
Query Match      80.0%; Score 14.4; DB 18; Length 25;
Best Local Similarity 72.2%; Pred. No. 94;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAYTGGGTNAAGTGNATH 18
   ||:|||||:|:|:|:|:|
Db 8 aactgggtgaatgtata 25

```

RESULT 10  
AAT36636  
ID AAT36636 standard; cDNA: 39 BP.  
XX  
XX AAT36636:  
AC AAT36636:

DT 17-NOV-1996 (first entry)  
 XX Interleukin-15 PCR primer NTFIL15B.  
 DE Interleukin-15; antagonist; mutein; graft versus host disease;  
 XX allograft; T-cell growth factor; polymerase chain reaction;  
 KW PCR; primer; ss.  
 XX Synthetic.  
 OS  
 XX MO9626274-A1.  
 PN 29-AUG-1996.  
 PD 21-FEB-1996; 96MO-US02520.  
 XX 22-FEB-1995; 95US-0392317.  
 PF 22-FEB-1995; 95US-0392317.  
 PR (IMMV ) IMMUNEX CORP.  
 XX Grabstein KH, Paxton RJ, Pettit DK;  
 PI WPI: 1996-402367/40.  
 DR Antagonists of Interleukin-15 - are used to treat patients having  
 XX symptoms of graft-versus-host disease and for prolonging allo-graft  
 PT survival  
 PT Example 1; Page 17; 32pp; English.  
 PS PCR primers NTFIL15B (AAT36636) and NCTFIL15F (AAT36637) are used  
 CC for the primary amplification of simian or human interleukin-15  
 CC DNA sequences (see also AAT36634-35), when maintenance of the  
 CC mature sequences is desired. A secondary amplification uses  
 CC primers that incorporate restriction sites into the amplified  
 CC sequence to allow incorporation of the product into yeast  
 CC expression vector palpaADH2. Other primers used for primary  
 CC PCR produce sequences coding for IL-15 muteins having amino acid  
 CC substitutions at positions D56 and/or Q156. Such muteins are  
 CC antagonists of IL-15 and can be used to treat graft-versus-host  
 CC disease and to prolong allograft survival.  
 CC  
 SO Sequence 39 BP; 12 A; 8 C; 9 G; 10 T; 0 other;  
 Query Match 80.0%; Score 14.4; DB 17; Length 39;  
 Best Local Similarity 72.2%; Pred. No. 99;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AATGGCTNAAYGTNATH 18  
 Db 22 aactgggtgaatgtaata 39  
 RESULT 11  
 AAT00525  
 ID AAT00525 standard; cDNA; 345 BP.  
 XX AAT00525;  
 AC 02-FEB-1996 (first entry)  
 DT Simian interleukin-15 mature polypeptide.  
 DE Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.  
 KW Cebus apella.  
 OS  
 XX Cebus apella.  
 FH Key Location/Qualifiers  
 FT CDS 1..345  
 FT /\*tag= a  
 FT /label= precursor nts 145-489  
 FT /note= "claimed"

XX MO952722-A.  
 PN 19-OCT-1995.  
 PD 06-APR-1994; 94MO-US03793.  
 XX 06-APR-1994; 94MO-US03793.  
 PF 06-APR-1994; 94MO-US03793.  
 PR (IMMV ) IMMUNEX CORP.  
 XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
 PI Rauch C;  
 PN WPI: 1995-373556/48.  
 DR P-PSDB; AAR83309.  
 DR Isolated DNA encoding polypeptide with mammalian IL-15 activity - which  
 XX stimulates proliferation and differentiation of T cells, used for  
 PT treating carcinoma(s), melanomas, etc. and viral infections  
 PT Claim 2; Page 26; 48pp; English.  
 PS A simian species of IL-15 (sIL-15) was purified and analysed by SDS-  
 CC PAGE. Bioassay of unstained gel slices indicated IL-15 activity was  
 CC assoc. with proteins having mol. wts in the range of 15-17 kDa. The  
 CC N-terminus of the 15-17 kDa was sequenced. The results indicated the  
 CC identity of the first 33 AAs of AAR83309. Subsequent sequencing of a  
 CC cDNA clone obtd. from a simian library provided a sequence encoding  
 CC the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA  
 CC leader sequence and a mature polypeptide AAR83309. The sequence of the  
 CC N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers  
 CC for the amplification of IL-15-specific DNA sequences. The first  
 CC 6 AAs of the N-terminus were used to design one primer, a  
 CC degenerate mixture coding for all possible codon usages - AAT00528.  
 CC The AA sequences of the simian mature N-terminus 26-31 were used  
 CC to design a second primer, a degenerate mixture coding for a  
 CC complement of all possible codon usages of AAs 26-31, omitting  
 CC posn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA  
 CC cells were used as templates. A 92 bp DNA fragment was used as a  
 CC hybridisation probe to screen a portion of a plasmid library contg.  
 CC cDNA inserts prep'd. from CV-1/EBNA polyadenylated RNA. This  
 CC resulted in the isolation of clone C85; sIL-15 that has an ORF  
 CC given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is  
 CC the precursor polypeptide. AAT00525 encodes the active polypeptide.  
 CC  
 SO Sequence 345 BP; 124 A; 50 C; 64 G; 107 T; 0 other;  
 Query Match 80.0%; Score 14.4; DB 16; Length 345;  
 Best Local Similarity 72.2%; Pred. No. 1.3e+02;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AATGGCTNAAYGTNATH 18  
 Db 1 aactgggtgaatgtaata 18  
 RESULT 12  
 AAT00527  
 ID AAT00527 standard; cDNA; 345 BP.  
 XX AAT00527;  
 AC 02-FEB-1996 (first entry)  
 DT Human interleukin-15 mature polypeptide.  
 DE Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.  
 KW Homo sapiens.  
 OS  
 XX Homo sapiens.  
 FH Key Location/Qualifiers

FT CDS 1..345  
 FT /\*tag= a  
 FT /label= corresp. to precursor nts 145-489  
 FT /note= "claimed"

XX MO9527722-A.  
 XX 19-OCT-1995.  
 XX 06-APR-1994; 94MO-US03793.  
 XX 06-APR-1994; 94MO-US03793.  
 XX (IMMV ) IMMUNEX CORP.  
 XX Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
 XX Rauch C;  
 XX WPI: 1995-373556/48.  
 XX P-PSDB: AAR83310.

XX Isolated DNA encoding polypeptide with mammalian IL-15 activity - which  
 XX stimulates proliferation and differentiation of T cells, used for  
 XX treating carcinoma(s), melanomas, etc. and viral infections  
 XX Claim 3; Page 28-29; 48pp; English.

XX A simian species of IL-15 (sIL-15) was purified and its AA  
 XX sequence and cDNA sequence analysed (see AAR83309, AAR83436,  
 XX AAT00524, AAT00525). Both the simian and the human ORFs encode  
 XX a precursor polypeptide (AAR83436, AAR83438). The precursor  
 XX polypeptides each comprise a 48-AA leader sequence and a sequence  
 XX encoding mature simian or human IL-15 polypeptides. The active  
 XX simian and human IL-15 polypeptides are disclosed in AAR83309 &  
 XX AAR83310 respectively. The invention also comprises other mammalian  
 XX IL-15, including human IL-15, that hybridise to probes defined by  
 XX AAR83438. A plasmid contg. a recombinant clone of human IL-15  
 XX cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 69245.  
 XX The deposit was named 141-hETF. AAR83435 is a mammalian mature  
 XX IL-15 polypeptide. It is a generic sequence which encompasses both  
 XX AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.  
 XX Sequence 345 BP; 121 A; 49 C; 68 G; 107 T; 0 other;

XX Query Match 80.0%; Score 14.4; DB 16; Length 345;  
 XX Best Local Similarity 72.2%; Pred. No. 1.3e+02;  
 XX Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGGTNAAYGTNATH 18  
 Db 1 aactggtgtaatgtaata 18

RESULT 13  
 AAF57024  
 ID AAF57024 standard; cDNA; 345 BP.  
 XX AAF57024;  
 XX 14-MAY-2001 (first entry)  
 XX Simian ETF (sETF) mature polypeptide encoding cDNA.  
 XX Epithelium-derived T-cell factor; ETF; simian; human; enteritis;  
 XX gastrointestinal disease; mucositis; peptic ulcer; cytostatic;  
 XX villus atrophic disorder; inflammatory bowel disease; antiinflammatory;  
 XX anti-HIV; antiviral; T-lymphocyte stimulator; ss.  
 XX Mammalia.  
 XX Key Location/Qualifiers  
 FT CDS 1..345

FT /\*tag= a  
 FT /product= "mature sETF"

XX US6184359-B1.  
 XX 06-FEB-2001.  
 XX 09-NOV-1998; 98US-0189193.  
 XX 22-FEB-1995; 95US-0393305.  
 XX 04-OCT-1996; 96US-0725969.  
 XX 08-MAR-1993; 93US-0031399.  
 XX 22-APR-1994; 94US-0233606.  
 XX (IMMV ) IMMUNEX CORP.  
 XX Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;  
 XX WPI: 2001-217801/22.  
 XX P-PSDB: AAB62013.

XX New antibodies that specifically binds epithelium-derived T-cell factor  
 XX polypeptide useful for e.g. treating or preventing gastrointestinal  
 XX diseases, HIV and HIV-associated diseases, augmenting destruction of  
 XX tumour cells -  
 XX Disclosure; Fig 1; 35pp; English.

XX The invention relates to simian and human epithelium-derived T-cell  
 XX factor (ETF) polypeptides. Antibodies that specifically bind to the ETF  
 XX polypeptides are used for treating or preventing gastrointestinal  
 XX diseases, such as chemotherapy and radiation therapy-induced enteritis  
 XX and mucositis, peptic ulcer disease, villus atrophic disorders and  
 XX inflammatory bowel disease; for increasing tolerated doses for radiation  
 XX therapy and chemotherapy agents which are limited by gastrointestinal  
 XX toxicity; and for treating HIV and HIV-associated diseases. The  
 XX antibodies are further used to treat a variety of other diseases or  
 XX conditions where it is desired to stimulate proliferation of  
 XX T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B  
 XX lymphocytes, to augment anti-infectious disease immunity, to induce CTL,  
 XX LAK or NK lytic activity, or to augment the destruction of tumour cells  
 XX or cells infected with virus. The present sequence represents a cDNA  
 XX encoding the simian ETF (sETF) mature polypeptide.

XX Sequence 345 BP; 121 A; 49 C; 68 G; 107 T; 0 other;

XX Query Match 80.0%; Score 14.4; DB 22; Length 345;  
 XX Best Local Similarity 72.2%; Pred. No. 1.3e+02;  
 XX Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGGTNAAYGTNATH 18  
 Db 1 aactggtgtaatgtaata 18

RESULT 14  
 AAF57025  
 ID AAF57025 standard; cDNA; 345 BP.  
 XX AAF57025;  
 XX 14-MAY-2001 (first entry)  
 XX Human ETF (hETF) mature polypeptide encoding cDNA.  
 XX Epithelium-derived T-cell factor; ETF; simian; human; enteritis;  
 XX gastrointestinal disease; mucositis; peptic ulcer; cytostatic;  
 XX villus atrophic disorder; inflammatory bowel disease; antiinflammatory;  
 XX anti-HIV; antiviral; T-lymphocyte stimulator; ss.  
 XX Homo sapiens.

FH Key Location/Qualifiers  
 FT CDS 1..345 /\*tag= a  
 FT /product= "mature hETF"  
 FT  
 PN US6184359-B1.  
 PN  
 PD 06-FEB-2001.  
 PD  
 XX 09-NOV-1998: 98US-0189193.  
 XX  
 XX 22-FEB-1995: 95US-0393305.  
 XX 04-OCT-1996: 96US-0725969.  
 XX 08-MAR-1993: 93US-0031399.  
 XX 22-APR-1994: 94US-0233606.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 XX Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;  
 XX  
 DR WPI: 2001-217801/22.  
 DR P-PSDB: AAB62015.  
 XX  
 PT New antibodies that specifically binds epithelium-derived T-cell factor  
 PT polypeptide useful for e.g. treating or preventing gastrointestinal  
 PT diseases, HIV and HTV-associated diseases, augmenting destruction of  
 PT tumour cells  
 PT  
 PS Disclosure: Fig 2: 35pp: English.  
 XX  
 XX The invention relates to stimian and human epithelium-derived T-cell  
 CC factor (ETF) polypeptides. Antibodies that specifically bind to the ETF  
 CC polypeptides are used for treating or preventing gastrointestinal  
 CC diseases, such as chemotherapy and radiation therapy-induced enteritis  
 CC and mucositis, peptic ulcer disease, villus atrophic disorders and  
 CC inflammatory bowel disease; for increasing tolerated doses for radiation  
 CC therapy and chemotherapy agents which are limited by gastrointestinal  
 CC toxicity; and for treating HIV and HTV-associated diseases. The  
 CC antibodies are further used to treat a variety of other diseases or  
 CC conditions where it is desired to stimulate proliferation of  
 CC T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B  
 CC lymphocytes, to augment anti-infectious disease immunity, to induce CTL,  
 CC LAK or NK lytic activity, or to augment the destruction of tumour cells  
 CC or cells infected with virus. The present sequence represents a CDNA  
 CC encoding the human ETF (hETF) mature polypeptide.  
 CC  
 XX Sequence 345 BP; 124 A; 50 C; 64 G; 107 T; 0 other;  
 SQ  
 Query Match 80.0%; Score 14.4; DB 22: Length 345;  
 Best Local Similarity 72.2%; Pred. No. 1.3e+02;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AAYTGGGTNAAYGTNATH 18  
 ||:||||| ||:|||||  
 Db 1 aactgggtgaatgtaata 18  
 RESULT 15  
 AAF21344  
 ID AAF21344 standard; DNA: 486 BP.  
 XX  
 AC AAF21344:  
 DT 14-MAR-2001 (first entry)  
 XX  
 DE Human low adenosine antisense oligonucleotide related sequence #2911.  
 XX  
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 PN WO200062736-A2.  
 PN  
 PD 26-OCT-2000.  
 PD  
 XX 24-MAR-2000: 2000WO-US08020.  
 XX  
 XX 06-APR-1999: 99US-0127958.  
 XX  
 XX (UYEC-) UNIV EAST CAROLINA.  
 XX (NYCE/) NYCE J W.  
 XX  
 PI Nyce JW;  
 XX  
 DR WPI: 2000-679539/66.  
 DR  
 PT Low adenosine (A) content antisense oligonucleotides which do not  
 PT trigger adenosine receptors during metabolism, useful e.g. for treating  
 PT cancers and respiratory obstructions  
 PT  
 PS Disclosure: Page 1348-1349; 1592pp: English.  
 XX  
 XX The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, central  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system peptide  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)  
 CC and/or surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention.  
 CC  
 XX Sequence 486 BP; 154 A; 81 C; 100 G; 151 T; 0 other;  
 SQ  
 Query Match 80.0%; Score 14.4; DB 21: Length 486;  
 Best Local Similarity 72.2%; Pred. No. 1.3e+02;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 AAYTGGGTNAAYGTNATH 18  
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 Db 123 aactgggtgaatgtaata 140



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RESULT 15
US-08-794-524-12/c
; Sequence 12, Application US/08794524
; Patent No. 5985262
; GENERAL INFORMATION:
; APPLICANT: Grabsteijn, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,524
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ. ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 345 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..345
; US-08-794-524-12

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Query Match      84.7%; Score 14.4; DB 2; Length 345;
Best Local Similarity 70.6%; Pred. No. 21;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACRRCCTCTCNGCTRTA 17
DB 92 ACATCACTTTCCTATA 76

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Search completed: June 19, 2002, 02:22:12  
Job time: 5420 sec

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaisters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 345 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..345  
US-08-726-817-13

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Best Local Similarity 70.6%; Pred. No. 21;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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DB 92 ACATCACTTCTGTATA 76

RESULT 13  
US-08-725-969-12/c  
Sequence 12, Application US/08725969  
Patent No. 5892001  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/725,969  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaisters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 345 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..345  
US-08-725-969-12

Query Match 84.7%; Score 14.4; DB 2; Length 345;  
Best Local Similarity 70.6%; Pred. No. 21;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRRCCTTCNGTCTA 17  
11:11:11:11:11:11  
DB 92 ACATCACTTCTGTATA 76

RESULT 14  
US-08-725-969-13/c  
Sequence 13, Application US/08725969  
Patent No. 5892001  
GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/725,969  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaisters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 345 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..345  
US-08-725-969-13

Query Match 84.7%; Score 14.4; DB 2; Length 345;  
Best Local Similarity 70.6%; Pred. No. 21;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRRCCTTCNGTCTA 17  
11:11:11:11:11:11  
DB 92 ACATCACTTCTGTATA 76

OY 1 ACRTGCTYTCNGTRTA 17  
11:11:11:11:11  
DB 92 ACATCACTTCCGTATA 76

## RESULT 10

US-08-393-305-13/c  
Sequence 13, Application US/08393305  
Patent No. 5574138  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/393,305  
FILING DATE: 22-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION/DOCKET NUMBER: 33,963  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 345 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..345  
US-08-393-305-13

Query Match 84.7%; Score 14.4; DB 1; Length 345;  
Best Local Similarity 70.6%; Pred. No. 21;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTGCTYTCNGTRTA 17  
11:11:11:11:11  
DB 92 ACATCACTTCCGTATA 76

## RESULT 11

US-08-726-817-12/c  
Sequence 12, Application US/08726817  
Patent No. 5707616  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,817  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION/DOCKET NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 345 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..345  
US-08-726-817-12

Query Match 84.7%; Score 14.4; DB 1; Length 345;  
Best Local Similarity 70.6%; Pred. No. 21;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTGCTYTCNGTRTA 17  
11:11:11:11:11  
DB 92 ACATCACTTCCGTATA 76

## RESULT 12

US-08-726-817-13/c  
Sequence 13, Application US/08726817  
Patent No. 5707616  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,817  
FILING DATE: 04-OCT-1996

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CORRESPONDENCE ADDRESS:
ADDRESS: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,193
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-189-193-11

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Best Local Similarity 84.7%; Score 14.4; DB 4; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACRTCRCTYTCNGTRTA 17

RESULT 8
PCT-US94-03793-11
Sequence 11, Application PC/TUS9403793
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Interleukin-15
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03793
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: launer, Charlene
REGISTRATION NUMBER: 33,035
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REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: YES
PCT-US94-03793-11

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACRTCRCTYTCNGTRTA 17

RESULT 9
US-08-393-305-12/C
Sequence 12, Application US/08393305
Patent No. 5574138
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,305
FILING DATE: 22-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..345
US-08-393-305-12

Query Match
Best Local Similarity 84.7%; Score 14.4; DB 1; Length 345;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
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REFERENCE/DOCKET NUMBER: 2811  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-504-042-11

Query Match 84.7%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACRTCTCTTCNGTCTTA 17

RESULT 5  
US-08-725-969-11  
Sequence 11, Application US/08725969

PATENT No. 5892001  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/725,969  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-725-969-11

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACRTCTCTTCNGTCTTA 17

RESULT 6  
US-08-794-524-11  
Sequence 11, Application US/08794524  
PATENT No. 5985262  
GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/794,524  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-794-524-11

Query Match 84.7%; Score 14.4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTCTTA 17  
|||||  
Db 1 ACRTCTCTTCNGTCTTA 17

RESULT 7  
US-09-189-193-11  
Sequence 11, Application US/09189193  
PATENT No. 6184359  
GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15

CITY: Seattle

NAME: Launer, Charlene  
REGISTRATION NUMBER: 33 025

CITY: Seattle

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 02:22:12 ; Search time 66.01 Seconds  
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Title: US-09-724-841-11

Perfect score: 17

Sequence: 1 ACRTCRCTTCNGTRTA 17

Scoring table: IDENTITY\_NUC  
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Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
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Listing first 45 summaries

Database : Issued Patents.NA.\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	14.4	84.7	17	1	US-08-393-305-11 Sequence 11, Appl
3	14.4	84.7	17	1	US-08-726-817-11 Sequence 11, Appl
4	14.4	84.7	17	1	US-08-504-042-11 Sequence 11, Appl
5	14.4	84.7	17	2	US-08-725-969-11 Sequence 11, Appl
6	14.4	84.7	17	2	US-08-794-524-11 Sequence 11, Appl
7	14.4	84.7	17	4	US-09-189-193-11 Sequence 11, Appl
8	14.4	84.7	17	5	PCR-US94-03793-11 Sequence 11, Appl
9	14.4	84.7	17	1	US-08-393-305-12 Sequence 12, Appl
10	14.4	84.7	17	1	US-08-726-817-12 Sequence 12, Appl
11	14.4	84.7	17	1	US-08-725-969-12 Sequence 12, Appl
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13	14.4	84.7	17	2	US-08-725-969-12 Sequence 12, Appl
14	14.4	84.7	17	2	US-08-794-524-12 Sequence 12, Appl
15	14.4	84.7	17	2	US-08-794-524-12 Sequence 12, Appl
16	14.4	84.7	17	2	US-08-794-524-12 Sequence 12, Appl
17	14.4	84.7	17	3	US-09-189-193-12 Sequence 12, Appl
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19	14.4	84.7	17	4	US-08-031-399-11 Sequence 13, Appl
20	14.4	84.7	17	1	US-08-031-399-11 Sequence 13, Appl
21	14.4	84.7	17	1	US-08-393-305-11 Sequence 13, Appl
22	14.4	84.7	17	1	US-08-393-305-11 Sequence 13, Appl
23	14.4	84.7	17	1	US-08-535-733-11 Sequence 13, Appl
24	14.4	84.7	17	1	US-08-726-817-11 Sequence 13, Appl
25	14.4	84.7	17	1	US-08-726-817-11 Sequence 13, Appl
26	14.4	84.7	17	1	US-08-504-042-11 Sequence 13, Appl
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C 30	14.4	84.7	489	2	US-08-725-969-1	Sequence 1, Appl1
C 31	14.4	84.7	489	2	US-08-725-969-1	Sequence 1, Appl1
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C 33	14.4	84.7	489	2	US-08-794-524-1	Sequence 1, Appl1
C 34	14.4	84.7	489	2	US-08-794-524-1	Sequence 1, Appl1
C 35	14.4	84.7	489	3	US-08-842-947-5	Sequence 5, Appl1
C 36	14.4	84.7	489	3	US-08-842-947-5	Sequence 7, Appl1
C 37	14.4	84.7	489	3	US-09-134-132-1	Sequence 1, Appl1
C 38	14.4	84.7	489	3	US-09-134-132-2	Sequence 2, Appl1
C 39	14.4	84.7	489	4	US-09-134-134A-1	Sequence 1, Appl1
C 40	14.4	84.7	489	4	US-09-134-134A-2	Sequence 2, Appl1
C 41	14.4	84.7	489	4	US-09-134-456-2	Sequence 1, Appl1
C 42	14.4	84.7	489	4	US-09-134-456-2	Sequence 2, Appl1
C 43	14.4	84.7	489	4	US-09-196-427-1	Sequence 1, Appl1
C 44	14.4	84.7	489	4	US-09-196-427-2	Sequence 2, Appl1
C 45	14.4	84.7	489	4	US-09-189-193-1	Sequence 1, Appl1
C 46	14.4	84.7	489	4	US-09-189-193-4	Sequence 4, Appl1

## ALIGNMENTS

RESULT 1  
US-08-031-399-11  
Sequence 11, Application US/08031399  
Patent No. 5552303  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: Epithelium-derived T-cell factor  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/031,399  
FILING DATE: 19930308  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Launer, Charlene  
REGISTRATION NUMBER: 33,035  
REFERENCE/DOCKET NUMBER: 2811  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
AMTI-SENSE: YES  
US-08-031-399-11

Query Match 84.7%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





SOURCE Tetraodon nigroviridis.  
 ORGANISM Tetraodon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 Tetraodontidae; Tetraodon.  
 REFERENCE 1 (bases 1 to 939)  
 AUTHORS Roest-Crolius,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C.,  
 Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and  
 Weissenbach,J.  
 TITLE Characterization and repeat analysis of the compact genome of the  
 freshwater pufferfish Tetraodon nigroviridis  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 939)  
 AUTHORS Roest-Crolius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,  
 Bernot,A., Fizames,C., Winkler,P., Brotlier,P., Quetier,F.,  
 Saurin,W. and Weissenbach,J.  
 TITLE Human gene number estimate provided by genome wide analysis using  
 Tetraodon nigroviridis DNA sequence  
 JOURNAL Unpublished  
 REFERENCE 3 (bases 1 to 939)  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases  
 COMMENT This sequence is a single read and was generated as part of a large  
 scale clone-end sequencing project of the Tetraodon nigroviridis  
 genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/Tetraodon>.  
 FEATURES  
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 Best Local Similarity 70.6%; Pred. No. 2e+03;  
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 Db 599 ACRTGCTCTGCTGTGA 583

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 Job time: 7369 sec

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 Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
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 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

## BASE COUNT

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 Best Local Similarity 70.6%; Pred. No. 1.9e+03;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCTCTTCNGRTA 17  
 11:11:11:11:11:11  
 Db 593 ACATCCTTCTCGTATA 609

RESULT 13  
 B1758686/c 872 bp mRNA linear EST 25-SEP-2001  
 LOCUS 603024240F1 NIH\_MGC\_114 Homo sapiens CDNA clone IMAGE:5194977 5',  
 DEFINITION mRNA sequence.  
 ACCESSION B1758686  
 VERSION B1758686.1 GI:15750264  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 872)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.llnl.gov  
 Plate: LLM11487 row: o column: 10  
 High quality sequence start: 24  
 Location/Qualifiers

## FEATURES

1. 872

/organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5194977"  
 /clone\_1lb="NIH\_MGC\_114"  
 /lab\_host="DH10B"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: EcoRV (destroyed); RNA source anonymous pool of 6  
 male brains, age range 23-27 yo. Library is oligo-dT  
 primed and directionally cloned (EcoRV site is destroyed  
 upon cloning). Average insert size 1.5 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 019. Note:  
 this is a NIH\_MGC Library."  
 BASE COUNT 200 a 222 c 227 g 223 t  
 ORIGIN

Query Match

84.7%; Score 14.4; DB 10; Length 872;

Best Local Similarity 70.6%; Pred. No. 1.9e+03;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCTCTTCNGRTA 17  
 11:11:11:11:11:11  
 Db 828 ACATCCTTCTCGTATA 812

RESULT 14  
 A2204912 935 bp DNA linear GSS 31-AUG-2000  
 LOCUS SP\_0097\_B2.G11.SPE Strongylocentrotus purpuratus, purple sea  
 urchin, sperm genomic BAC library Strongylocentrotus purpuratus  
 genomic clone Plate=97 Col=22 Row=N, DNA sequence.  
 ACCESSION A2204912  
 VERSION A2204912.1 GI:8399832  
 KEYWORDS GSS.  
 SOURCE Strongylocentrotus purpuratus.  
 ORGANISM Strongylocentrotus purpuratus.  
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 Echinoidae; Euechinoidae; Echinacea; Echinoida;  
 Strongylocentrotidae; Strongylocentrotus.  
 1 (bases 1 to 935)  
 Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Blondi,T.R.,  
 Swartzell,S., Wallace,J.C., Rouska,A.J., Livingston,B.T., Wray,  
 G.A., Eitensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and  
 Hood,L.  
 A sea urchin genome project: Sequence scan, virtual map, and  
 additional resources  
 Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)  
 20402566  
 COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L  
 Division of Biology 156-29  
 California Institute of Technology  
 Pasadena California 91125, USA  
 Tel: (626) 395-8421  
 Fax: (626) 793-3047  
 Email: acameron@caltech.edu  
 Plate: 97 row: N column: 22  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 935.  
 Location/Qualifiers

## FEATURES

1. 935

/organism="Strongylocentrotus purpuratus"  
 /db\_xref="taxon:7668"  
 /clone="Plate=97 Col=22 Row=N"  
 /clone\_1lb="Strongylocentrotus purpuratus, purple sea  
 urchin, sperm genomic BAC library"  
 /note="Organ: sperm; Vector: BACs 6; BAC Clones in E-Coli  
 DH10B"  
 BASE COUNT 261 a 171 c 170 g 333 t  
 ORIGIN

Query Match 84.7%; Score 14.4; DB 12; Length 935;  
 Best Local Similarity 70.6%; Pred. No. 2e+03;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCTCTTCNGRTA 17  
 11:11:11:11:11:11  
 Db 497 ACATCCTTCTCGTATA 513

RESULT 15  
 CNS02YU0/c 939 bp DNA linear GSS 15-MAY-2000  
 LOCUS Tetradon nigroviridis genome survey sequence pUC-Or1 end of clone  
 181k04 of library G from Tetradon nigroviridis, genomic survey  
 sequence.  
 ACCESSION CNS02YU0  
 VERSION AL220113  
 AL220113.1 GI:7878932  
 KEYWORDS GSS; genome survey sequence.

Library constructed by Life Technologies. Investigator  
 providing samples: Gilbert Smith, NIH

BASE COUNT 139 a 280 c 179 g 193 t

Query Match 84.7%; Score 14.4; DB 10; Length 791;  
 Best Local Similarity 70.6%; Pred. No. 1.8e+03;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCRCTTCNGTGA 17  
 11:11:11:11:11:11

Db 530 ACATCACTCTCTGTGA 546

RESULT 10  
 BG184658 800 bp mRNA linear EST 21-APR-2001  
 LOCUS BG184658  
 DEFINITION RST3720 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
 ACCESSION BG184658  
 VERSION BG184658.1 GI:13706473  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 800)  
 Harrington,J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,  
 Cain,S., Leventhal,C., Thornton,M., Ramchandran,R., Whittington,J.,  
 Lerner,L., Costanzo,D., Mcelligott,K., Booser,S., Mays,R., Smith,  
 'E., Veloso,N., Kika,A., Hess,J., Cotlren,K., Lo,K., Offenbacher,  
 'J., Danzig,J. and Ducar,M.  
 Creation of genome-wide protein expression libraries using random  
 activation of gene expression  
 Nat. Biotechnol. 19 (5), 440-445 (2001)

TITLE  
 JOURNAL MEDLINE  
 COMMENT  
 Contact: Scott J. Cain  
 Athersys, Inc.  
 3201 Carnegie Ave, Cleveland, OH 44115, USA  
 Tel: 216 431 9900  
 Fax: 216 361 9596  
 Email: scai@atersys.com  
 High quality sequence stop: 444.

FEATURES  
 Source  
 Location/Qualifiers  
 1..800  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="Athersys RAGE Library"  
 /cell\_line="HT1080"  
 /note="See 'Creation of Genome-wide Protein Expression  
 Libraries using Random Activation of Gene Expression',  
 Nature Biotechnology, in press. Note that even though the  
 cell type indicated is HT1080, since a random activation  
 method was used, these sequence tags are not necessarily  
 expressed in HT1080 under normal circumstances."

BASE COUNT 235 a 151 c 165 g 247 t

Query Match 84.7%; Score 14.4; DB 10; Length 800;  
 Best Local Similarity 70.6%; Pred. No. 1.8e+03;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCRCTTCNGTGA 17  
 11:11:11:11:11:11

Db 500 ACATCACTTCGTGA 484

RESULT 11  
 BH551681 816 bp DNA linear GSS 14-DEC-2001  
 LOCUS BH551681  
 DEFINITION B0GLV81TR B0GL Brassica oleracea genomic clone B0GLV81, DNA  
 sequence.

ACCESSION BH551681  
 VERSION BH551681.1 GI:17803461  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea.  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 816)  
 Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 unpublished (2001)  
 JOURNAL Other GSS: B0GLV81TF  
 COMMENT Contact: Chris Town

TIGR Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TR  
 Class: sheared ends.  
 Location/Qualifiers  
 1..816  
 /organism="Brassica oleracea"  
 /strain="T01000DH3"  
 /db\_xref="taxon:3712"  
 /clone\_lib="B0GLV81"  
 /clone\_lib="B0GLV81"  
 /note="Vector: PHOS1; Site 1: BstXI; 2-3 kb sheared  
 genomic DNA inserted into PHOS1 using BstXI linkers"

BASE COUNT 257 a 192 c 176 g 191 t

Query Match 84.7%; Score 14.4; DB 12; Length 816;  
 Best Local Similarity 70.6%; Pred. No. 1.9e+03;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCRCTTCNGTGA 17  
 11:11:11:11:11:11

Db 530 ACATCACTCTCTGTGA 514

RESULT 12  
 BG167809 823 bp mRNA linear EST 06-FEB-2001  
 LOCUS BG167809  
 DEFINITION 602333995P1 NIH\_MGC\_89 Homo sapiens cDNA clone IMAGE:4447957 5',  
 mRNA sequence.

ACCESSION BG167809  
 VERSION BG167809.1 GI:12674512  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 823)  
 NIH-MGC http://mgi.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strusberg, Ph.D.  
 Email: cga@bbs-remail.nih.gov  
 Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LLM10229 row: 1 column: 14  
 High quality sequence stop: 645.  
 Location/Qualifiers  
 1..823

FEATURES  
 Source

BG675661  
 LOCUS 756 bp mRNA linear EST 01-MAY-2001  
 DEFINITION 60262072F1 NCI\_CGAP\_Skn4 Homo sapiens cDNA clone IMAGE:4747265 5',  
 mRNA sequence.  
 ACCESSION BG675661  
 VERSION BG675661.1 GI:13907057  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 756)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: James Cleaver, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM10596 row: p column: 18  
 High quality sequence stop: 745.  
 Location/Qualifiers  
 1..756  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="IMAGE:4747265"  
 /clone\_lib="NCI\_CGAP\_Skn4"  
 /tissue\_type="squamous cell carcinoma"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NCI;  
 Site\_2: Sall; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.5kb. Library constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."  
 BASE COUNT 221 a 147 c 168 g 220 t  
 ORIGIN  
 Query Match 84.7% Score 14.4; DB 10; Length 756;  
 Best Local Similarity 70.6% Pred. No. 1.8e+03;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 ACRTGCTCTTCGCTGTA 17  
 ||:||||:||||:||||  
 Db 710 ACATCAGCTTCAGTATA 726  
 RESULT 8  
 BI832895 756 bp mRNA linear EST 04-OCT-2001  
 LOCUS 603082478F1 NIH\_MGC\_120 Homo sapiens cDNA clone IMAGE:5221771 5',  
 mRNA sequence.  
 ACCESSION BI832895  
 VERSION BI832895.1 GI:15944445  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 756)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM11557 row: k column: 20  
 High quality sequence stop: 756.  
 Location/Qualifiers  
 1..756  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="IMAGE:5221771"  
 /clone\_lib="NIH\_MGC\_120"  
 /lab\_host="DH10B"  
 /note="Organ: pooled pancreas and spleen; Vector:  
 pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
 source anonymous pool of spleen and pancreas from 28 yo  
 male. Library is oligo-dT primed and directionally cloned  
 (EcoRV site is destroyed upon cloning). Average insert  
 size 1.5 kb. Insert size range 1-2.5 kb. Library is  
 normalized and enriched for full-length clones and was  
 constructed by C. Gruber (Invitrogen). Research Genetics  
 tracking code 025. Note: this is a NIH-MGC Library."  
 BASE COUNT 247 a 115 c 143 g 251 t  
 ORIGIN  
 Query Match 84.7% Score 14.4; DB 10; Length 756;  
 Best Local Similarity 70.6% Pred. No. 1.8e+03;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 ACRTGCTCTTCGCTGTA 17  
 ||:||||:||||:||||  
 Db 63 ACATCAGCTTCGCTATA 47  
 RESULT 9  
 BE380693 791 bp mRNA linear EST 21-JUL-2000  
 LOCUS 601270690F1 NCI\_CGAP\_Mam1 Mus musculus cDNA clone IMAGE:3599950 5',  
 mRNA sequence.  
 ACCESSION BE380693  
 VERSION BE380693.1 GI:9325968  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 REFERENCE 1 (bases 1 to 791)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM8783 row: c column: 23  
 High quality sequence stop: 51.  
 Location/Qualifiers  
 1..791  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone\_image="IMAGE:3599950"  
 /clone\_lib="NCI\_CGAP\_Mam1"  
 /tissue\_type="tumor, biopsy sample"  
 /dev\_stage="10 months, virgin"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: Sall;  
 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-remail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraiki  
 Toshlyuki and Piero Carninci (RIKEN)  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLM10752 row: 0 column: 20  
 High quality sequence stop: 630.  
 Location/Qualifiers

## FEATURES

## Source

1..643  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="4830955"  
 /clone\_lib="NIH\_MGC\_97"  
 /lab\_host="DH10B"  
 /note="Organ: testis; Vector: pBluescriptR (modified  
 pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcgag  
 ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',  
 size-selected for average insert size 2.2 kb and  
 normalized to R0F 5. This is a primary library enriched  
 for full-length clones and constructed using the  
 cap-trapper method (Carninci, In preparation). Library  
 constructed by M. Brownstein (NIH/NHGRI, National  
 Institutes of Health). Note: this is a NIH\_MGC Library."

## BASE COUNT

161 a 165 c 160 g 157 t

## ORIGIN

Query Match 84.7%; Score 14.4; DB 10; Length 643;  
 Best Local Similarity 70.6%; Pred. No. 1.7e+03;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATCCTCTCCGTATA 17

Db 340 ACATCCTCTCCGTATA 324

RESULT 5 673 bp mRNA linear EST 17-JUL-2001  
 AU211793

LOCUS AU211793 unpublished oligo-capped cDNA library, stage L2  
 DEFINITION Caenorhabditis elegans cDNA clone yk776g02 3', mRNA sequence.

ACCESSION AU211793

VERSION AU211793.1 GI:14849331

KEYWORDS EST.

SOURCE Caenorhabditis elegans.

ORGANISM Caenorhabditis elegans.

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae  
 1 (bases 1 to 673)

AUTHORS Kohara,Y., Shih-I.T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.  
 and Sugano,S.

REFERENCE A complementary view of the C.elegans genome

AUTHORS Unpublished (2001)

JOURNAL Contact: Yuji Kohara

COMMENT Genome Biology Lab.

National Institute of Genetics  
 Yata 1111, Mishima, Shizuoka 411, Japan  
 Tel: 81-559-81-6854  
 Fax: 81-559-81-6855

EMAIL: ykohara@lab.nig.ac.jp.

location/Qualifiers

1..673

/organism="Caenorhabditis elegans"

/strain="N2"

/db\_xref="taxon:6239"

/clone="yk776g02"

/clone\_lib="unpublished oligo-capped cDNA library, stage

L2"

/sex="Hermaphrodite"

/tissue\_type="whole animal"

/dev\_stage="L2"

BASE COUNT 188 a 139 c 125 g 219 t 2 others

## ORIGIN

Query Match 84.7%; Score 14.4; DB 9; Length 673;  
 Best Local Similarity 70.6%; Pred. No. 1.7e+03;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATCCTCTCCGTATA 17

Db 455 ACATCCTCTCCGTATA 471

RESULT 6 735 bp DNA linear GSS 03-NOV-2001  
 AG091422

LOCUS Pan troglodytes DNA, clone: PTB-091E11.R, genomic survey sequence.

DEFINITION AG091422

ACCESSION AG091422.1 GI:16643224

VERSION GSS: GSS (genome survey sequence).

KEYWORDS Pan troglodytes male lymphoblast DNA, clone\_lib:PTB Chimpanzee Male

SOURCE BAC library clone:PTB-091E11.R.

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE 1 (sites)

Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

Totoki,Y., Watanabe,H. and Sakaki,Y.

BAC end sequences of library PTB

Unpublished

2 (bases 1 to 735)

Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Submitted (02-NOV-2001) Asao Fujiyama, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suenro-chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/

Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end

was generated during the R&D process and may have higher chance of

clone tracking errors.

PRIMERS

Sequencing: M13Rev

LIBRARY

Vector : PKS145

R.Site 1 : SacI

R.Site 2 : SacI

Location/Qualifiers

1..735

/organism="Pan troglodytes"

/db\_xref="taxon:9598"

/clone="PTB-091E11.R"

/sex="male"

/cell\_type="lymphoblast"

/clone\_lib="PTB Chimpanzee Male BAC Library"

BASE COUNT 239 a 184 c 95 g 217 t

ORIGIN

Query Match 84.7%; Score 14.4; DB 12; Length 735;

Best Local Similarity 70.6%; Pred. No. 1.8e+03;

Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACATCCTCTCCGTATA 17

Db 211 ACATCCTCTCCGTATA 227

RESULT 7

/lab\_host="DH10B"  
/note="Organ: mixed (see below); Vector: pT73D-Pac  
(Pharmacia) with a modified polylinker; Site\_1: Not I;  
Site\_2: Eco RI; Equal amounts of plasmid DNA from three  
normalized libraries (melanocyte 2NDH, pregnant uterus  
NBHPU, and fetal heart NBH19W) were mixed, and ss circles  
were made in vitro. Following HAP purification, this DNA  
was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from pools of  
5,000 clones made from the same 3 libraries. The pools  
consisted of I.M.A.G.E. clones 260232-265223,  
340488-345479, and 484488-489479."

BASE COUNT 149 a 91 c 108 g 161 t

ORIGIN

Query Match 84.7%; Score 14.4; DB 9; Length 509;  
Best Local Similarity 70.6%; Pred. No. 1.5e+03;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTRCTYTCNGRTA 17  
11:11:11:11 11:11

DB 340 ACATCACTTCCTGATA 324

RESULT 2  
LOCUS A1860008 637 bp mRNA linear EST 07-MAR-2000  
DEFINITION wm22g03.x1 NCI\_CGAP\_Ut4 Homo sapiens cDNA clone IMAGE:2436724 3'  
similar to SW:IL15\_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ; mRNA  
sequence.  
ACCESSION A1860008  
VERSION A1860008.1 GI:5513624  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 637)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaaps-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Greg Lennon, Ph.D.  
Cloned through the I.M.A.G.E. Consortium/LNL at:  
www.bio.lnl.gov/dbtr/image/image.html  
Insert Length: 3944 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 410.

FEATURES  
Source  
1..637  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2436724"  
/clone\_lib="NCI\_CGAP\_Ut4"  
/tissue\_type="serous papillary carcinoma, high grade, 2  
pooled tumors"  
/lab\_host="DH10B"  
/note="Organ: uterus; Vector: PCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.48 kb. Life Technologies catalog #:  
11542-016"

BASE COUNT 207 a 111 c 91 g 227 t 1 others

ORIGIN

Query Match 84.7%; Score 14.4; DB 9; Length 637;  
Best Local Similarity 70.6%; Pred. No. 1.7e+03;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTRCTYTCNGRTA 17  
11:11:11:11 11:11

DB 591 ACATCACTTCCTGATA 607

RESULT 3  
LOCUS BJ144320 641 bp mRNA linear EST 23-JAN-2002  
DEFINITION BJ144320 unpublished oligo-capped cDNA library, C. elegans L1 stage  
Caenorhabditis elegans cDNA clone yk1205h10 3', mRNA sequence.  
ACCESSION BJ144320  
VERSION BJ144320.1 GI:18304486  
KEYWORDS EST.  
SOURCE Caenorhabditis elegans.  
ORGANISM Caenorhabditis elegans.

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae  
; Rhabditidae; Peleodermidae; Caenorhabditis.  
1 (bases 1 to 641)  
AUTHORS Kohara, Y., Shin, I.T., Thierry-Mieg, J., Thierry-Mieg, D., Suzuki, Y.  
and Sugano, S.  
TITLE A complementary view of the C.elegans genome  
JOURNAL Unpublished (2002)  
COMMENT Contact: Tadasi Shin-I  
Center for Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshin@genetics.nig.ac.jp.

FEATURES  
Source  
1..641  
Location/Qualifiers

/organism="Caenorhabditis elegans"  
/strain="N2"  
/db\_xref="taxon:6239"  
/clone="yk1205h10"  
/clone\_lib="unpublished oligo-capped cDNA library, C.  
elegans L1 stage"  
/sex="hermaphrodite"  
/tissue\_type="whole animal"  
/dev\_stage="L1"

BASE COUNT 183 a 133 c 114 g 209 t 2 others

ORIGIN

Query Match 84.7%; Score 14.4; DB 10; Length 641;  
Best Local Similarity 70.6%; Pred. No. 1.7e+03;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTRCTYTCNGRTA 17  
11:11:11:11 11:11

DB 443 ACATCACTTCCTGATA 459

RESULT 4  
LOCUS BG722010 643 bp mRNA linear EST 08-MAY-2001  
DEFINITION BG722010 NIH\_MGC\_97 Homo sapiens cDNA clone IMAGE:4830955 5',  
mRNA sequence.  
ACCESSION BG722010  
VERSION BG722010.1 GI:14001197  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 643)  
AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 02:15:53 ; Search time 2591.91 Seconds  
(without alignments)  
88.525 Million cell updates/sec

Title: US-09-724-841-11

Perfect score: 17

Sequence: 1 ACRTCCRYTCNGTRTA 17

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthm:\*
- 3: em\_estln:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hlc:\*
- 9: gb\_estl:\*
- 10: gb\_estl2:\*
- 11: gb\_hlc:\*
- 12: gb\_gss:\*
- 13: em\_gss\_hum:\*
- 14: em\_gss\_inv:\*
- 15: em\_gss\_pln:\*
- 16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
C	1	14.4	84.7	509	9	AA463370	zx97d12.r	AA463370 zx97d12.r
C	2	14.4	84.7	637	9	AI860008	wm22903.x	AI860008 wm22903.x
C	3	14.4	84.7	641	10	BJ144320	BJ144320	BJ144320 BJ144320
C	4	14.4	84.7	643	10	BG722010	602698780	BG722010 602698780
C	5	14.4	84.7	673	9	AU211793	AU211793	AU211793 AU211793
C	6	14.4	84.7	735	12	AG091422	Pan trogl	AG091422 Pan trogl
C	7	14.4	84.7	756	10	BG675661	603622072	BG675661 603622072
C	8	14.4	84.7	756	10	BI832895	603082478	BI832895 603082478
C	9	14.4	84.7	791	10	BE380693	601270690	BE380693 601270690
C	10	14.4	84.7	800	10	BG184658	RST3720.A	BG184658 RST3720.A
C	11	14.4	84.7	816	12	BH551681	BOGLV81TR	BH551681 BOGLV81TR
C	12	14.4	84.7	823	10	BG167809	602339953	BG167809 602339953
C	13	14.4	84.7	872	10	BI758686	603024240	BI758686 603024240
C	14	14.4	84.7	935	12	AZ204912	SP_0097_B	AZ204912 SP_0097_B
C	15	14.4	84.7	939	12	CNS02Y00	Tetraodon	AZ20113 Tetraodon
C	16	14.4	84.7	973	9	BB612210	BB612210	BB612210 BB612210
C	17	14.4	84.7	982	9	AL548180	AL548180	AL548180 AL548180

C	18	14.4	84.7	989	12	CNS065ZW	AL13922.T7 end of	AL13922.T7 end of
C	19	14.4	84.7	994	9	AL572832	AL572832	AL572832
C	20	14.4	84.7	1039	10	BG111302	BG111302	BG111302
C	21	14.4	84.7	1937	10	BE686933	BE686933	BE686933
C	22	13.4	78.8	169	10	R30748	R30748	R30748
C	23	13.4	78.8	190	10	BG000197	BG000197	BG000197
C	24	13.4	78.8	192	12	AO647900	AO647900	AO647900
C	25	13.4	78.8	237	12	A2737501	A2737501	A2737501
C	26	13.4	78.8	254	9	AV209229	AV209229	AV209229
C	27	13.4	78.8	259	9	AI573986	AI573986	AI573986
C	28	13.4	78.8	273	9	AI578096	AI578096	AI578096
C	29	13.4	78.8	273	9	AM530109	AM530109	AM530109
C	30	13.4	78.8	284	9	AA684293	AA684293	AA684293
C	31	13.4	78.8	285	9	AV155882	AV155882	AV155882
C	32	13.4	78.8	289	9	AA762984	AA762984	AA762984
C	33	13.4	78.8	294	9	AV339187	AV339187	AV339187
C	34	13.4	78.8	307	10	BG608621	BG608621	BG608621
C	35	13.4	78.8	307	10	BM483899	BM483899	BM483899
C	36	13.4	78.8	308	9	AM786829	AM786829	AM786829
C	37	13.4	78.8	328	12	AO651927	AO651927	AO651927
C	38	13.4	78.8	337	10	BM484651	BM484651	BM484651
C	39	13.4	78.8	335	9	AU203535	AU203535	AU203535
C	40	13.4	78.8	360	9	AV187535	AV187535	AV187535
C	41	13.4	78.8	360	9	AV195907	AV195907	AV195907
C	42	13.4	78.8	369	9	AA826842	AA826842	AA826842
C	43	13.4	78.8	374	10	BM133541	BM133541	BM133541
C	44	13.4	78.8	378	10	BE692792	BE692792	BE692792
C	45	13.4	78.8	390	12	AQ166959	AQ166959	AQ166959

## ALIGNMENTS

RESULT 1  
AA463370/c  
LOCUS  
DEFINITION  
AA463370 509 bp mRNA linear EST 10-JUN-1997  
zx97d12.r1 Soares\_NHMPu\_S1 Homo sapiens cDNA clone IMAGE:811703 5'  
similar to SW:IL15\_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ; mRNA  
sequence.

ACCESSION  
AA463370  
VERSION  
AA463370.1 GI:2188254

KEYWORDS  
EST.  
SOURCE  
human.

ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
1 (bases 1 to 509)  
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,  
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,  
Schellenberg, R., Steptoe, M., Tan, F., Theisling, B., White, Y., Wyllie,  
T., Waterston, R. and Wilson, R.  
Washu-Merck EST Project 1997

TITLE  
Unpublished (1997)

JOURNAL  
Contact: Wilson RK  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

COMMENT  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Possible reversed clone: similarity on wrong strand  
Seq primer: -28m13 rev2 ET from Amersham  
High quality sequence stop: 416.

FEATURES  
source  
1..509  
/organism="Homo sapiens"  
/db\_xref="GDB:6042614"  
/db\_xref="taxon:9606"  
/clone="IMAGE:811703"  
/clone\_lib="Soares\_NHMPu\_S1"  
/tissue\_type="Pooled human melanocyte, fetal heart, and  
pregnant uterus"





CC leader sequence and a mature polypeptide AAR83309. The sequence of the  
 CC N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers  
 CC for the amplification of IL-15-specific DNA sequences. The first  
 CC 6 AAs of the N-terminus were used to design one primer, a  
 CC degenerate mixture coding for all possible codon usages - AAT00528.  
 CC The AA sequences of the simian mature N-terminus 26-31 were used  
 CC to design a second primer, a degenerate mixture coding for a  
 CC complement of all possible codon usages of AAs 26-31, omitting  
 CC posn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA  
 CC cells were used as templates. A 92 bp DNA fragment was used as a  
 CC hybridization probe to screen a portion of a plasmid library contg.  
 CC cDNA inserts prep'd. from CV-1/EBNA polyadenylated RNA. This  
 CC resulted in the isolation of clone C85-STL-15 that has an ORF  
 CC given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is  
 CC the precursor polypeptide.  
 XX

SQ Sequence 489 BP; 162 A; 81 C; 92 G; 154 T; 0 other;

Query Match 84.7%; Score 14.4; DB 16; Length 489;  
 Best Local Similarity 70.6%; Pred. No. 1.1e+02;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTGRCCTGCTGTRTA 17  
 ||:||||:||||:|  
 DB 236 ACATCAGTTCTGTATTA 220

Search completed: June 19, 2002, 02:20:52  
 Job time: 5410 sec



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RESULT 12
AAAF57025/C
ID AAF57025 standard; cDNA; 345 BP.
XX
AC AAF57025;
XX
DT 14-MAY-2001 (first entry)
XX
DE Human ETF (hETF) mature polypeptide encoding cDNA.
XX
KM Epithelium-derived T-cell factor; ETF; simian; human; enteritis;
KM gastrointestinal disease; mucositis; peptic ulcer; cytostatic;
KM villus atrophic disorder; inflammatory bowel disease; antiinflammatory;
KM anti-HIV; antiviral; T-lymphocyte stimulator; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..345
FT /tag= a
FT /product= "mature hETF"
FT
XX
PN US6184359-B1.
XX
PD 06-FEB-2001.
XX
PF 09-NOV-1998; 98US-0189193.
XX
PR 22-FEB-1995; 95US-0393305.
PR 04-OCT-1996; 96US-0725969.
PR 08-MAR-1993; 93US-0031399.
PR 22-APR-1994; 94US-0233606.
XX
PA (IMV) IMMUNEX CORP.
XX
PI Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;
XX
DR WPI: 2001-217801/22.
DR P-PSDB; AAB62015.
XX
XX
PT New antibodies that specifically binds epithelium-derived T-cell factor
PT polypeptide useful for e.g. treating or preventing gastrointestinal
PT diseases, HIV and HIV-associated diseases, augmenting destruction of
PT tumour cells -
XX
XX
PS Disclosure; Fig 2; 35pp; English.
XX
XX
CC The invention relates to simian and human epithelium-derived T-cell
CC factor (ETF) polypeptides. Antibodies that specifically bind to the ETF
CC polypeptides are used for treating or preventing gastrointestinal
CC diseases, such as chemotherapy and radiation therapy-induced enteritis
CC and mucositis, peptic ulcer disease, villus atrophic disorders and
CC inflammatory bowel disease; for increasing tolerated doses for radiation
CC therapy and chemotherapy agents which are limited by gastrointestinal
CC toxicity; and for treating HIV and HIV-associated diseases. The
CC antibodies are further used to treat a variety of other diseases or
CC conditions where it is desired to stimulate proliferation of
CC T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B
CC lymphocytes, to augment anti-infectious disease immunity, to induce CTL,
CC LAK or NK lytic activity, or to augment the destruction of tumour cells
CC or cells infected with virus. The present sequence represents a cDNA
CC encoding the human ETF (hETF) mature polypeptide.
XX
SQ Sequence 345 BP; 124 A; 50 C; 64 G; 107 T; 0 other;

```

```

Query Match      84.7%; Score 14.4; DB 22; Length 345;
Best Local Similarity 70.6%; Pred. No. 1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 ACRTGCTGTCGCTGTA 17
   |||:|||||:|||||
Db 92 ACATCACTTCTGTATA 76

```

```

RESULT 13
AAAF21344/C
ID AAF21344 standard; DNA; 486 BP.
XX
AC AAF21344;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2911.
XX
XX
KM Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KM human; airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; anasthmatic; analgesic; hypotensive; cytostatic;
KM respiratory obstruction; pulmonary vasoconstriction; impeded respiration;
KM surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000MO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PA (UYEC/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI: 2000-679539/66.
XX
XX
PT Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
XX
PS Disclosure; Page 1348-1349; 1592pp; English.
XX
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, anasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide

```

```

RESULT 10
AAT00527/c
ID AAT00527 standard; cDNA: 345 BP.
XX
XX AAT00527:
XX
AC 02-FEB-1996 (first entry)
XX
XX
DE Human interleukin-15 mature polypeptide.
XX
XX Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 1..345
FT /*tag= a
FT /label= corresp. to precursor nts 145-489
FT /note= "claimed"
XX
XX
PN M09527722-A.
XX
PD 19-OCT-1995.
XX
PF 06-APR-1994; 94WO-US03793.
XX
PR 06-APR-1994; 94WO-US03793.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI Rauch C;
XX
XX WPI: 1995-373556/48.
XX
XX P-PSDB: AAR83310.
XX
XX
XX Isolated DNA encoding polypeptide with mammalian IL-15 activity - which
PT stimulates proliferation and differentiation of T cells, used for
PT treating carcinoma(s), melanomas, etc. and viral infections
XX
XX
XX Claim 3; Page 28-29; 48pp; English.
XX
XX A simian species of IL-15 (sIL-15) was purified and its AA
CC sequence and cDNA sequence analysed (see AAR83309, AAR83436,
CC AAT00524, AAT00525). Both the simian and the human ORFs encode
CC a precursor polypeptide (AAR83436, AAR83438). The precursor
CC polypeptides each comprise a 48-AA leader sequence and a sequence
CC encoding mature simian or human IL-15 polypeptides. The active
CC simian and human IL-15 polypeptides are disclosed in AAR83309 &
CC AAR83310 respectively. The invention also comprises other mammalian
CC IL-15, including human IL-15, that hybridise to probes defined by
CC AAR83438. A plasmid contg. a recombinant clone of human IL-15
CC cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 69245.
CC The deposit was named 141-hETF. AAR83435 is a mammalian mature
CC IL-15 polypeptide. It is a generic sequence which encompasses both
CC AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.
XX
XX
SQ Sequence 345 BP; 121 A; 49 C; 68 G; 107 T; 0 other;

```

```

Query Match 84.7%; Score 14.4; DB 16; Length 345;
Best Local Similarity 70.6%; Pred. No. 1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 ACRTRCTYTCNGTRTA 17
   11:11:11:11:11:11
DB 92 ACATCACTTCCGTATA 76

```

```

RESULT 11
AAF57024/c

```

```

ID AAF57024 standard; cDNA: 345 BP.
XX
XX AAF57024;
XX
AC 14-MAY-2001 (first entry)
XX
XX
DE Simian ETF (SETF) mature polypeptide encoding cDNA.
XX
XX
XX Epithelium-derived T-cell factor; ETF; simian; human; enteritis;
XX gastrointestinal disease; mucositis; peptic ulcer; cytostatic;
XX villus atrophic disorder; inflammatory bowel disease; antiinflammatory;
XX anti-HIV; antiviral; T-lymphocyte stimulator; ss.
XX
OS Mammalia.
XX
FH Key Location/Qualifiers
FT 1..345
FT /*tag= a
FT /product= "mature setf"
XX
XX
PN US6184359-B1.
XX
PD 06-FEB-2001.
XX
PF 09-NOV-1998; 98US-0189193.
XX
PR 22-FEB-1995; 95US-0393305.
PR 04-OCT-1996; 96US-0725968.
PR 08-MAR-1993; 93US-0031399.
PR 22-APR-1994; 94US-0233606.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX
XX Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;
XX
XX
XX WPI: 2001-217801/22.
XX
XX P-PSDB: AAB62013.
XX
XX
XX New antibodies that specifically binds epithelium-derived T-cell factor
PT polypeptide useful for e.g. treating or preventing gastrointestinal
PT diseases, HIV and HIV-associated diseases, augmenting destruction of
PT tumour cells -
XX
XX
XX Disclosure: Fig 1; 35pp; English.
XX
XX
XX The invention relates to simian and human epithelium-derived T-cell
CC factor (ETF) polypeptides. Antibodies that specifically bind to the ETF
CC polypeptides are used for treating or preventing gastrointestinal
CC diseases, such as chemotherapy and radiation therapy-induced enteritis
CC and mucositis, peptic ulcer disease, villus atrophic disorders and
CC inflammatory bowel disease; for increasing tolerated doses for radiation
CC therapy and chemotherapy agents which are limited by gastrointestinal
CC toxicity; and for treating HIV and HIV-associated diseases. The
CC antibodies are further used to treat a variety of other diseases or
CC conditions where it is desired to stimulate proliferation of
CC T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B
CC lymphocytes, to augment anti-infectious disease immunity, to induce CTL,
CC LAK or NK lytic activity, or to augment the destruction of tumour cells
CC or cells infected with virus. The present sequence represents a cDNA
CC encoding the simian ETF (SETF) mature polypeptide.
XX
XX
SQ Sequence 345 BP; 121 A; 49 C; 68 G; 107 T; 0 other;

```

```

Query Match 84.7%; Score 14.4; DB 22; Length 345;
Best Local Similarity 70.6%; Pred. No. 1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

OY 1 ACRTRCTYTCNGTRTA 17
   11:11:11:11:11:11
DB 92 ACATCACTTCCGTATA 76

```

## RESULT 8

ID AAF57023 standard; DNA; 17 BP.

AC AAF57023;

DT 14-MAY-2001 (first entry)

DE Simian ETF cDNA specific degenerate primer.

KW Epithelium-derived T-cell factor; ETF; simian; human; enteritis;

KW gastrointestinal disease; mucositis; peptic ulcer; cytostatic;

KW villus atrophic disorder; inflammatory bowel disease; antiinflammatory;

KW anti-HIV; antiviral; T-lymphocyte stimulator; PCR primer; ss.

OS Synthetic.

PN US6184359-B1.

PD 06-FEB-2001.

PF 09-NOV-1998; 98US-0189193.

PR 22-FEB-1995; 95US-0393305.

PR 04-OCT-1996; 96US-0725969.

PR 08-MAR-1993; 93US-0031399.

PR 22-APR-1994; 94US-0233606.

PA (IMMV) IMMUNEX CORP.

PI Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;

DR WPI; 2001-217801/22.

XX New antibodies that specifically binds epithelium-derived T-cell factor

XX polypeptide useful for e.g. treating or preventing gastrointestinal

XX diseases, HIV and HIV-associated diseases, augmenting destruction of

XX tumour cells -

XX Example 3; Column 25; 35pp; English.

XX The invention relates to simian and human epithelium-derived T-cell

XX factor (ETF) polypeptides. Antibodies that specifically bind to the ETF

XX polypeptides are used for treating or preventing gastrointestinal

XX diseases, such as chemotherapy and radiation therapy-induced enteritis

XX and mucositis, peptic ulcer disease, villus atrophic disorders and

XX inflammatory bowel disease; for increasing tolerated doses for radiation

XX therapy and chemotherapy agents which are limited by gastrointestinal

XX toxicity; and for treating HIV and HIV-associated diseases. The

XX antibodies are further used to treat a variety of other diseases or

XX conditions where it is desired to stimulate proliferation of

XX T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B

XX lymphocytes, to augment anti-infectious disease immunity, to induce CTL,

XX LAK or NK lytic activity, or to augment the destruction of tumour cells

XX or cells infected with virus. Sequences AAF57021-23 represent PCR primers

XX used for simian ETF (SETF) cDNA cloning.

XX Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

XX Query Match 84.7%; Score 14.4; DB 22; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 71;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTCTCTGCTGTTA 17

DB 1 acrtctctgctgtrta 17

RESULT 9

AAT00525/C

ID AAT00525 standard; cDNA; 345 BP.

AC AAT00525;

DT 02-FEB-1996 (first entry)

DE Simian interleukin-15 mature polypeptide.

KW Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.

OS Cebus apella.

FH Key Location/Qualifiers

FT CDS 1..345

FT /tag= a

FT /label= precursor nts 145-489

FT /note= "Claimed"

PN W09527722-A.

PD 19-OCT-1995.

PF 06-APR-1994; 94WO-US03793.

PR 06-APR-1994; 94WO-US03793.

PA (IMMV) IMMUNEX CORP.

PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;

DR P-PSDB; AAR83309.

XX WPI: 1995-373556/48.

XX Isolated DNA encoding polypeptide with mammalian IL-15 activity - which

XX stimulates proliferation and differentiation of T cells, used for

XX treating carcinoma(s), melanomas, etc. and viral infections

XX Claim 2; Page 26; 48pp; English.

XX A simian species of IL-15 (sIL-15) was purified and analysed by SDS-

XX PAGE. Bioassay of unstained gel slices indicated IL-15 activity was

XX assoc. with proteins having mol. wts in the range of 15-17 kDa. The

XX N-terminus of the 15-17 kDa was sequenced. The results indicated the

XX identity of the first 33 AAs of AAR83309. Subsequent sequencing of a

XX cDNA clone obtd. from a simian library provided a sequence encoding

XX the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA

XX leader sequence and a mature polypeptide AAR83309. The sequence of the

XX N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers

XX for the amplification of IL-15-specific DNA sequences. The first

XX 6 AAs of the N-terminus were used to design one primer, a

XX degenerate mixture coding for all possible codon usages - AAT00528.

XX The AA sequences of the simian mature N-terminus 26-31 were used

XX to design a second primer, a degenerate mixture coding for a

XX complement of all possible codon usages of AAs 26-31, omitting

XX posn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA

XX cells were used as templates. A 92 bp DNA fragment was used as a

XX hybridisation probe to screen a portion of a plasmid library contg.

XX cDNA inserts prepd. from CV-1/EBNA polyadenylated RNA. This

XX resulted in the isolation of clone C85.sIL-15 that has an ORF

XX given in AAT00524. AAR83309 is the active polypeptide &amp; AAR83436 is

XX the precursor polypeptide. AAT00525 encodes the active polypeptide.

XX

XX

XX Sequence 345 BP; 124 A; 50 C; 64 G; 107 T; 0 other;

XX Query Match 84.7%; Score 14.4; DB 16; Length 345;

XX Best Local Similarity 70.6%; Pred. No. 1e+02;

XX Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTCTCTGCTGTTA 17

DB 92 ACATCACTTCTGTATA 76

AA29485  
ID AAX29485 standard; DNA; 17 BP.  
XX  
AC AAX29485;  
XX  
DT 10-JUN-1999 (first entry)  
XX  
DE Simian ETF DNA amplifying primer.  
XX  
KW Epithelium-derived T-cell factor; ETF; immunoassay; enteritis; ulcer;  
KW T cell proliferation; gastrointestinal disease; mucositis; colitis;  
KW gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease;  
KW human immune deficiency virus; tumour; simian; PCR primer; ss.  
XX  
OS Synthetic.  
XX  
PN US5892001-A.  
XX  
PD 06-APR-1999.  
XX  
PE 04-OCT-1996; 96US-0725969.  
XX  
PF 22-FEB-1995; 95US-0393305.  
PR 08-MAR-1993; 93US-0031399.  
PR 22-APR-1994; 94US-0233606.  
PR 04-OCT-1996; 96US-0725969.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
PI Rauch C;  
XX  
DR WPI: 1999-253930/21.  
XX  
PT Antibodies specific for epithelium-derived T-cell growth factor  
XX  
PS Example 3; Columns 25; 34pp; English.  
XX  
CC The invention relates to an isolated antibody that binds specifically to  
CC a simian or human epithelium-derived T-cell factor (ETF) polypeptide.  
CC The antibodies are used, optionally when immobilized or labeled, to  
CC detect and quantify ETF in standard immunoassays. They may also be used  
CC as diagnostic and therapeutic agents, e.g. when conjugated to toxins (or  
CC their precursors) or radionuclides. ETF induces proliferation and/or  
CC differentiation of T cells (or their precursors), e.g. for use in  
CC establishing long term in vitro cultures; and is also used to treat  
CC gastrointestinal disease (e.g. enteritis or mucositis induced by  
CC chemotherapy or radiation, peptide ulcer, gastroenteritis, colitis,  
CC villus atrophy, malignancy and inflammatory bowel disease), to treat  
CC human immune deficiency virus infection or associated disease, or  
CC generally in any situation requiring stimulation of T or B cell  
CC proliferation, secretion of immunoglobulins or certain cytokines,  
CC increased anti-infectious disease immunity, induction of T-cell lytic  
CC activity or increased destruction of tumour or virus-infected cells.  
CC Sequences AAX29483-85 represent primers for PCR amplification of the  
CC simian ETF DNA sequences.  
XX  
SO Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 20; Length 17;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRRCCTTCNGTTRTA 17  
DB 1 acrtcrctylcngtrta 17  
|||||

RESULT 7  
AA238248  
ID AAX238248 standard; DNA; 17 BP.  
XX

AA238248;  
AC  
XX  
DT 09-FEB-2000 (first entry)  
XX  
DE Simian ETF degenerate PCR primer #11.  
XX  
KW ETF; epithelium-derived T-cell factor; T-cell; T-lymphocyte;  
KW proliferation; differentiation; epithelium; cell culture; treatment; HIV;  
KW CD8+; gastrointestinal disease; gastroenteritis; colitis;  
KW gastrointestinal disease; gastroenteritis; colitis;  
KW inflammatory bowel disease; villus atrophic disorder; enteritis;  
KW chemotherapy; radiotherapy; gut toxicity; cancer; side effect;  
KW tolerated dose; PCR; primer; ss.  
XX  
OS Synthetic.  
XX  
PN Mammalia.  
XX  
PD US5985262-A.  
XX  
PE 16-NOV-1999.  
XX  
PF 03-FEB-1997; 97US-0794524.  
XX  
PR 22-FEB-1995; 95US-0393305.  
PR 04-OCT-1996; 96US-0726817.  
PR 08-MAR-1993; 93US-0031399.  
PR 22-APR-1994; 94US-0233606.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;  
PI P-PSDB; AAY52313.  
XX  
DR WPI: 2000-022267/02.  
XX  
PT Stimulation of T-cells in human immunodeficiency virus infected  
PT patients -  
XX  
PS Example 3; Column 25; 33pp; English.  
XX  
CC This sequence represents simian ETF degenerate PCR primer #11,  
CC used with degenerate primer #9 (AA238246) to amplify a fragment  
CC of the gene encoding simian epithelium-derived T-cell factor (ETF).  
CC This was used to probe a simian cDNA library for a clone with a  
CC complete open reading frame (AA238224). The primers were based on  
CC N-terminal amino acid sequences in the purified ETF protein.  
CC ETF is a previously unidentified T-cell growth factor which  
CC stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to  
CC proliferate and differentiate. It also promotes proliferation of the  
CC gastrointestinal epithelium. The protein can be used to promote long-term  
CC in vitro culture of T-lymphocytes and T-cell lines. ETF can be used for  
CC treating HIV infection, HIV-associated diseases, and other diseases or  
CC conditions where stimulation of T-cell proliferation would be desirable  
CC e.g., it could be used to augment the destruction of tumour cells or  
CC virally-infected cells. ETF may also be used to treat or prevent  
CC gastrointestinal disease, including chemotherapy and radiotherapy  
CC associated enteritis, gastroenteritis, colitis, inflammatory bowel  
CC disease and villus atrophic disorders. Chemotherapy and radiotherapy  
CC associated enteritis (gut toxicity) results in bleeding and sepsis due to  
CC gastrointestinal flora entering the blood, and thus can limit the dosage  
CC of therapeutic agent administered to a cancer patient. ETF may therefore  
CC be used to increase the tolerated doses radiotherapy and chemotherapy.  
XX  
SO Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 21; Length 17;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRRCCTTCNGTTRTA 17  
DB 1 acrtcrctylcngtrta 17  
|||||

CC CV1/EBNA cDNA library for the full-length SEF coding sequence.  
CC Mature SEF induces proliferation and/or differentiation of precursor  
CC or mature T cells and is useful for promoting long-term in vitro  
CC culture of T-lymphocytes and T-cell lines. It is used for treating  
CC gastrointestinal diseases including peptic ulcer, colitis and  
CC malignancy and for treating HIV infection.  
XX  
SQ Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 17; Length 17;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTCTTA 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 acrtctctctcngtrta 17

## RESULT 4

AAV42246  
ID AAV42246 standard; DNA; 17 BP.

XX  
AC AAT42246;

XX  
DT 05-FEB-1997 (first entry)

XX  
DE Simian ETF gene primer #2 based on amino acids 26-31 of mature ETF.

XX  
KW Epithelium-derived T-cell factor; simian; human; culture; proliferation;  
KW epithelial cell; differentiation; T-lymphocyte; African green monkey;  
KW primer; PCR; polymerase chain reaction; amplification; probe; ss.

XX  
OS Synthetic.

XX  
PN US5552303-A.

XX  
PD 03-SEP-1996.

XX  
PF 08-MAR-1993; 93US-0031399.

XX  
PR 08-MAR-1993; 93US-0031399.

XX  
PA (IMMV) IMMUNEX CORP.

XX  
PI Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;

XX  
DR WPI: 1996-412063/41.

XX  
PT New isolated simian and human epithelium-derived T-cell factors -  
PT which stimulate the proliferation and/or differentiation of  
PT T-lymphocytes and T-cell lines

XX  
PS Example 3; Column 17; 22pp; English.

XX  
CC Primers AAT42244-6 were used to amplify a 92 bp fragment of the African  
CC green monkey epithelium-derived T-cell factor (ETF; AAT42243). The  
CC sequence of this primer is based on amino acids 26-31 of the mature ETF  
CC protein sequence obtained by peptide sequencing the purified protein.  
CC The template for the amplification was cDNA derived from monkey kidney  
CC CV-1/EBNA cells stimulated to proliferate by phorbol 12-myristate  
CC 13-acetate. The 92 bp fragment was labelled and used as a probe to  
CC isolate a clone c85.ETF which contained the simian gene. ETF is a  
CC protein of 15-17 kD which is expressed by epithelial cells and  
CC stimulates proliferation and/or differentiation of precursor and/or  
CC mature T cells. The protein is therefore useful for promoting long term  
CC in vivo culture of T-lymphocytes and T-cell lines.

XX  
SQ Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 17; Length 17;  
Best Local Similarity 100.0%; Pred. No. 71;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTCTTA 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 acrtctctctcngtrta 17

## RESULT 5

AAV02877  
ID AAV02877 standard; DNA; 17 BP.

XX  
AC AAV02877;

XX  
DT 08-MAY-1998 (first entry)

XX  
DE Simian epithelium derived T-cell factor PCR primer 3.

XX  
KW Epithelium derived T-cell factor; ETF; simian; gastrointestinal disease;  
KW B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;  
KW treatment; prevention; PCR primer; ss.

XX  
OS Synthetic.

XX  
PN US5707616-A.

XX  
PD 13-JAN-1998.

XX  
PF 04-OCT-1996; 96US-0726817.

XX  
PR 22-FEB-1995; 95US-0393305.

XX  
PR 08-MAR-1993; 93US-0031399.

XX  
PR 22-APR-1994; 94US-0233606.

XX  
PA (IMMV) IMMUNEX CORP.

XX  
PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;

XX  
PT Rauch C;

XX  
PT Treatment or prevention of gastrointestinal diseases - by  
PT administering epithelium-derived T-cell factor polypeptide

XX  
PS Example 3; Column 43-44; 34pp; English.

XX  
CC PCR primers AAV02875-V02877 are used in the amplification of a simian  
CC epithelium-derived T-cell factor (ETF) which is used in a method for  
CC treating or preventing gastrointestinal disease. These polypeptides have  
CC particular application in the treatment of gastrointestinal disorders  
CC associated with disruption of the gastrointestinal epithelium or villi  
CC such as chemotherapy- and radiation-therapy induced enteritis (gut  
CC toxicity), mucositis, peptic ulcer disease, gastroenteritis and colitis,  
CC villus atrophic disorders, malignancy and inflammatory bowel disease.  
CC ETF polypeptides may also be useful in the treatment of human  
CC immunodeficiency virus (HIV) and HIV-associated disease due to their  
CC ability to stimulate CD4+ and CD8+ cells. Biologically active ETF may be  
CC used to treat a variety of other diseases or conditions where T-cell or  
CC B-cell stimulation is desired.

XX  
SQ Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 19; Length 17;  
Best Local Similarity 100.0%; Pred. No. 71;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTCTTA 17  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 acrtctctctcngtrta 17

RESULT 6



XX DR WPI; 1995-373556/48.  
 XX  
 PT Isolated DNA encoding polypeptide with mammalian IL-15 activity - which  
 PT stimulates proliferation and differentiation of T cells, used for  
 PT treating carcinoma(s), melanomas, etc. and viral infections  
 XX  
 PS Example: Page 21; 48pp; English.  
 XX  
 CC A simian species of IL-15 (sIL-15) was purified and analysed by SDS-  
 CC PAGE. Bioassay of unstained gel slices indicated IL-15 activity was  
 CC assoc. with proteins having mol. wts in the range of 15-17 kDa. The  
 CC N-terminus of the 15-17 kDa was sequenced. The results indicated the  
 CC identity of the first 33 AAs of AAR83309. Subsequent sequencing of a  
 CC cDNA clone obtd. from a simian library provided a sequence encoding  
 CC the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA  
 CC leader sequence and a mature polypeptide AAR83309. The sequence of the  
 CC N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers  
 CC for the amplification of IL-15-specific DNA sequences. The first  
 CC 6 AAs of the N-terminus were used to design one primer, a  
 CC degenerate mixture coding for all possible codon usages - AAT00528.  
 CC The AA sequences of the simian mature N-terminus 26-31 were used  
 CC to design a second primer, a degenerate mixture coding for a  
 CC complement of all possible codon usages of AAs 26-31, omitting  
 CC post. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA  
 CC cells were used as templates. A 92 bp DNA fragment was used as a  
 CC hybridisn. probe to screen a portion of a plasmid library contg.  
 CC cDNA inserts prep. from CV-1/EBNA polyadenylated RNA. This  
 CC resulted in the isolation of clone G85. sIL-15 that has an ORF  
 CC given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is  
 CC the precursor polypeptide.  
 XX  
 SQ Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 16; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 71;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTRCTYTCNGTRPA 17  
 ||||||||||||||||  
 Db 1 acrtcrctytcngtrta 17

RESULT 2  
 AA084587  
 ID AA084587 standard; cDNA; 17 BP.  
 XX  
 AC AA084587;  
 XX  
 DT 04-SEP-1995 (first entry)  
 XX  
 DE Simian IL-15 primer.  
 XX  
 KW Interleukin-15; IL-15; sIL-15; T-cell growth factor;  
 KW African green monkey; CV-1; antitumor; virucide; primer; PCR;  
 KW polymerase chain reaction; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN ZA9402636-A.  
 XX  
 PD 28-DEC-1994.  
 XX  
 PF 18-APR-1994; 94ZA-0002636.  
 XX  
 PR 18-APR-1994; 94ZA-0002636.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
 PI Rauch C;

DR WPI; 1995-082473/11.  
 XX  
 PT New purified interleukin-15 - which induces T cell proliferation  
 PT and differentiation, used for the treatment of tumours and viral  
 PT infection  
 XX  
 PS Example 3; Page 21; 47pp; English.  
 XX  
 CC cDNA generated from PMA-stimulated CV-1/EBNA cells was amplified  
 CC by PCR using primers (AA084585-87) based on the N-terminal sequence  
 CC of simian interleukin-15 (sIL-15). A clone encoding sIL-15 was  
 CC obtained (AA084583).  
 XX  
 SQ Sequence 17 BP; 2 A; 4 C; 1 G; 5 T; 5 other;

Query Match 84.7%; Score 14.4; DB 16; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 71;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTRCTYTCNGTRPA 17  
 ||||||||||||||||  
 Db 1 acrtcrctytcngtrta 17

RESULT 3  
 AAT49459  
 ID AAT49459 standard; cDNA; 17 BP.  
 XX  
 AC AAT49459;  
 XX  
 DT 11-MAR-1997 (first entry)  
 XX  
 DE Epithelium derived T cell factor PCR primer.  
 XX  
 KW Simian epithelium derived T cell factor; sETF; African green monkey;  
 KW Cercopithecus aethiops; CV1/EBNA cell; T-cell; B-cell; lymphocyte;  
 KW proliferation; differentiation; gastrointestinal; HIV infection;  
 KW human immunodeficiency virus; polymerase chain reaction; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5574138-A.  
 XX  
 PD 12-NOV-1996.  
 XX  
 PR 08-MAR-1993; 93US-0031399.  
 XX  
 PR 22-FEB-1995; 95US-0393305.  
 XX  
 PR 08-MAR-1993; 93US-0031399.  
 XX  
 PR 22-APR-1994; 94US-0233606.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
 PI Rauch C;  
 XX  
 DR WPI; 1996-517923/51.  
 XX  
 PT New epithelium derived T cell factor - induces proliferation of T  
 PT and B cells, stimulates destruction of tumour and virus-infected  
 PT cells and protects against toxicity, partic. for treating intestinal  
 PT disease and HIV infection  
 XX  
 PS Example 3; Column 25; 35pp; English.  
 XX  
 CC The simian ETF (epithelium derived T cell factor) was isolated from  
 CC African green monkey CV1/EBNA cell conditioned medium. The N-  
 CC terminal sequence of the purified sETF was determined and then PCR  
 CC primers were designed based on the sequence information. The  
 CC present sequence is that of a degenerate primer based on amino acids  
 CC 26-31, i.e. Tyr-Thr-Glu-Ser-Asp-Val. A 92 bp fragment was  
 CC amplified from CV1/EBNA DNA and was used as a probe to screen a





BASE COUNT 146 a 75 c 87 g 145 t  
ORIGIN

Query Match 84.7%; Score 14.4; DB 9; Length 453;  
Best Local Similarity 70.6%; Pred. No. 7.1e+02;  
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTGCTCTGNGRRRA 17  
11:11:11:11:11:11  
Db 202 ACATCACTTCCGTATA 186

Search completed: June 19, 2002, 02:54:34  
Job time: 7092 sec

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FEATURES
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              /organism="unknown"
BASE COUNT   121 a 49 c 68 g 107 t
ORIGIN

Query Match      84.7%; Score 14.4; DB 6; Length 345;
Best Local Similarity 70.6%; Pred. No. 7.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTATA 17
   11:11:11:11:11:11
Db 92 ACATCACTTTCCTATA 76

RESULT 12
LOCUS 128857 345 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 13 from patent US 5574138.
ACCESSION 128857
VERSION 128857.1 GI:1819641
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 345)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Epithelium-derived T-cell factor
JOURNAL Patent: US 5574138-A 13 12-NOV-1996;
FEATURES
  source      Location/Qualifiers
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              /organism="unknown"
BASE COUNT   124 a 50 c 64 g 107 t
ORIGIN

Query Match      84.7%; Score 14.4; DB 6; Length 345;
Best Local Similarity 70.6%; Pred. No. 7.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTATA 17
   11:11:11:11:11:11
Db 92 ACATCACTTTCCTATA 76

RESULT 13
LOCUS 179226 345 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 12 from patent US 5707616.
ACCESSION 179226
VERSION 179226.1 GI:3207516
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 345)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method for treating or preventing gastrointestinal disease with
epithelium-derived T-cell factor
JOURNAL Patent: US 5707616-A 12 13-JAN-1998;
FEATURES
  source      Location/Qualifiers
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              /organism="unknown"
BASE COUNT   121 a 49 c 68 g 107 t
ORIGIN

Query Match      84.7%; Score 14.4; DB 6; Length 345;
Best Local Similarity 70.6%; Pred. No. 7.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTATA 17

```

```

Db 92 ACATCACTTTCCTATA 76
   11:11:11:11:11:11

RESULT 14
LOCUS 179227 345 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 13 from patent US 5707616.
ACCESSION 179227
VERSION 179227.1 GI:3207517
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 345)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method for treating or preventing gastrointestinal disease with
epithelium-derived T-cell factor
JOURNAL Patent: US 5707616-A 13 13-JAN-1998;
FEATURES
  source      Location/Qualifiers
              1..345
              /organism="unknown"
BASE COUNT   124 a 50 c 64 g 107 t
ORIGIN

Query Match      84.7%; Score 14.4; DB 6; Length 345;
Best Local Similarity 70.6%; Pred. No. 7.1e+02;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACRTCTCTTCNGTATA 17
   11:11:11:11:11:11
Db 92 ACATCACTTTCCTATA 76

RESULT 15
LOCUS HS115MR 453 bp mRNA linear PRI 26-SEP-1995
DEFINITION H.sapiens mRNA for Interleukin 15 (partial).
ACCESSION Z38000
VERSION Z38000.1 GI:995656
KEYWORDS Interleukin; Interleukin-15.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 111 to 452)
AUTHORS SOREL,M.A. and Jacques,Y.
TITLE IL15 expression in human keratinocytes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 453)
AUTHORS SOREL,M.A.
TITLE Direct Submersion
JOURNAL Submitted (03-OCT-1994) Michel A Sorel, Institut de biologie,
INSERM U 211, 9 Quai de Moncousu, Nantes, 44035, FRANCE
FEATURES
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              /isolate="INDIVIDUAL"
              /db_xref="taxon:9606"
              /sex="Male"
              /cell_type="HUMAN KERATINOCYTES FROM FORESKIN"
              /tissue_type="EPIDERMAL TISSUE"
              111..452
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              /db_xref="GI:995657"
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LEI0VLSLSDASIHDTVENLLIILANNSLSSNGNVTESGCKCELELEKNIKEFIQS

```

## ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGCTTCNGTCTATA 17  
 |||:|||||:|||||:|  
 Db 1 ACRTGCTTCNGTCTATA 17

RESULT 7  
 LOCUS AR070288 345 bp DNA linear PAT 18-FEB-2000  
 DEFINITION Sequence 12 from patent US 5892001.  
 ACCESSION AR070288  
 VERSION AR070288.1 GI:7221176  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 345)  
 AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
 TITLE Epithelium-derived T-cell factor antibodies  
 JOURNAL Patent: US 5892001-A 12 06-APR-1999;  
 FEATURES Location/Qualifiers  
 source 1..345

BASE COUNT 121 a 49 c 68 g 107 t  
 ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 345;  
 Best Local Similarity 70.6%; Pred. No. 7.1e+02;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTGCTTCNGTCTATA 17  
 |||:|||||:|||||:|  
 Db 92 ACATCCTTCCTGATA 76

RESULT 8  
 LOCUS AR070289 345 bp DNA linear PAT 18-FEB-2000  
 DEFINITION Sequence 13 from patent US 5892001.  
 ACCESSION AR070289  
 VERSION AR070289.1 GI:7221177  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 345)  
 AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
 TITLE Epithelium-derived T-cell factor antibodies  
 JOURNAL Patent: US 5892001-A 13 06-APR-1999;  
 FEATURES Location/Qualifiers  
 source 1..345

BASE COUNT 124 a 50 c 64 g 107 t  
 ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 345;  
 Best Local Similarity 70.6%; Pred. No. 7.1e+02;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTGCTTCNGTCTATA 17  
 |||:|||||:|||||:|  
 Db 92 ACATCCTTCCTGATA 76

RESULT 9

AR085747/c 345 bp DNA linear PAT 07-SEP-2000  
 LOCUS AR085747  
 DEFINITION Sequence 12 from patent US 5985262.  
 ACCESSION AR085747  
 VERSION AR085747.1 GI:10012513  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 345)  
 AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
 TITLE Method of treatment with epithelium derived T-cell factor  
 JOURNAL Patent: US 5985262-A 12 16-NOV-1999;  
 FEATURES Location/Qualifiers  
 source 1..345

BASE COUNT 121 a 49 c 68 g 107 t  
 ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 345;  
 Best Local Similarity 70.6%; Pred. No. 7.1e+02;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTGCTTCNGTCTATA 17  
 |||:|||||:|||||:|  
 Db 92 ACATCCTTCCTGATA 76

RESULT 10  
 LOCUS AR085748 345 bp DNA linear PAT 07-SEP-2000  
 DEFINITION Sequence 13 from patent US 5985262.  
 ACCESSION AR085748  
 VERSION AR085748.1 GI:10012514  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 345)  
 AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
 TITLE Method of treatment with epithelium derived T-cell factor  
 JOURNAL Patent: US 5985262-A 13 16-NOV-1999;  
 FEATURES Location/Qualifiers  
 source 1..345

BASE COUNT 124 a 50 c 64 g 107 t  
 ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 345;  
 Best Local Similarity 70.6%; Pred. No. 7.1e+02;  
 Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 ACRTGCTTCNGTCTATA 17  
 |||:|||||:|||||:|  
 Db 92 ACATCCTTCCTGATA 76

RESULT 11  
 LOCUS I28856 345 bp DNA linear PAT 06-FEB-1997  
 DEFINITION Sequence 12 from patent US 5574138.  
 ACCESSION I28856  
 VERSION I28856.1 GI:1819640  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 345)  
 AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
 TITLE Epithelium-derived T-cell factor  
 JOURNAL Patent: US 5574138-A 12 12-NOV-1996;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACRTCRCTYTCNGTRTA 17  
 |||||  
 Db 1 ACRTCRCTYTCNGTRTA 17

RESULT 2  
 AR070287 17 bp DNA linear PAT 18-FEB-2000  
 LOCUS Sequence 11 from patent US 5892001.  
 DEFINITION AR070287  
 ACCESSION AR070287  
 VERSION AR070287.1 GI:7221175  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
 TITLE Epithelium-derived T-cell factor antibodies  
 JOURNAL Patent: US 5892001-A 11 06-APR-1999;  
 FEATURES Location/Qualifiers  
 source 1..17  
 BASE COUNT 2 a 4 c 1 g 5 t 5 others  
 ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACRTCRCTYTCNGTRTA 17  
 |||||  
 Db 1 ACRTCRCTYTCNGTRTA 17

RESULT 3  
 AR085746 17 bp DNA linear PAT 07-SEP-2000  
 LOCUS Sequence 11 from patent US 5985262.  
 DEFINITION AR085746  
 ACCESSION AR085746  
 VERSION AR085746.1 GI:10012512  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
 TITLE Method of treatment with epithelium derived T-cell factor  
 JOURNAL Patent: US 5985262-A 11 16-NOV-1999;  
 FEATURES Location/Qualifiers  
 source 1..17  
 BASE COUNT 2 a 4 c 1 g 5 t 5 others  
 ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACRTCRCTYTCNGTRTA 17  
 |||||  
 Db 1 ACRTCRCTYTCNGTRTA 17

RESULT 4  
 I25788 17 bp DNA linear PAT 07-OCT-1996  
 LOCUS Sequence 11 from patent US 5552303.  
 DEFINITION I25788  
 ACCESSION I25788  
 VERSION I25788.1 GI:1605658

KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Grabstein,K.H., Anderson,D., Eisenman,J., Fung,V. and Rauch,C.  
 TITLE DNA encoding epithelium-derived T-cell factor  
 JOURNAL Patent: US 5552303-A 11 03-SEP-1996;  
 FEATURES Location/Qualifiers  
 source 1..17  
 BASE COUNT 2 a 4 c 1 g 5 t 5 others  
 ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACRTCRCTYTCNGTRTA 17  
 |||||  
 Db 1 ACRTCRCTYTCNGTRTA 17

RESULT 5  
 I28855 17 bp DNA linear PAT 06-FEB-1997  
 LOCUS Sequence 11 from patent US 5574138.  
 DEFINITION I28855  
 ACCESSION I28855  
 VERSION I28855.1 GI:1819638  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
 TITLE Epithelium-derived T-cell factor  
 JOURNAL Patent: US 5574138-A 11 12-NOV-1996;  
 FEATURES Location/Qualifiers  
 source 1..17  
 BASE COUNT 2 a 4 c 1 g 5 t 5 others  
 ORIGIN

Query Match 84.7%; Score 14.4; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ACRTCRCTYTCNGTRTA 17  
 |||||  
 Db 1 ACRTCRCTYTCNGTRTA 17

RESULT 6  
 I79225 17 bp DNA linear PAT 10-JUN-1998  
 LOCUS Sequence 11 from patent US 5707616.  
 DEFINITION I79225  
 ACCESSION I79225  
 VERSION I79225.1 GI:3207515  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
 TITLE Method for treating or preventing gastrointestinal disease with  
 epithelium-derived T-cell factor  
 JOURNAL Patent: US 5707616-A 11 13-JAN-1998;  
 FEATURES Location/Qualifiers  
 source 1..17  
 BASE COUNT 2 a 4 c 1 g 5 t 5 others

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 02:54:34 ; Search time 1924.67 Seconds  
(without alignments)  
184.837 Million cell updates/sec

Title: US-09-724-841-11

Perfect score: 17

Sequence: 1 ACRTCRCTTCNGTRTA 17

Scoring table: IDENTITY\_NUC

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*  
1: gb.ba:\*  
2: gb.htg:\*  
3: gb.in:\*  
4: gb.om:\*  
5: gb.ov:\*  
6: gb.pat:\*  
7: gb.ph:\*  
8: gb.pl:\*  
9: gb.pr:\*  
10: gb.ro:\*  
11: gb.sts:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vi:\*  
15: em.ba:\*  
16: em.fun:\*  
17: em.hum:\*  
18: em.in:\*  
19: em.mu:\*  
20: em.om:\*  
21: em.or:\*  
22: em.ov:\*  
23: em.pat:\*  
24: em.ph:\*  
25: em.pl:\*  
26: em.ro:\*  
27: em.sts:\*  
28: em.un:\*  
29: em.vi:\*  
30: em.htg.hum:\*  
31: em.htg.liv:\*  
32: em.htg.other:\*  
33: em.htgo.liv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result Query 8  
No. Score Match Length DB ID Description

1	14.4	84.7	17	6	AR004273	AR004273 Sequence
2	14.4	84.7	17	6	AR070287	AR070287 Sequence
3	14.4	84.7	17	6	AR085746	AR085746 Sequence
4	14.4	84.7	17	6	125788	125788 Sequence 11
5	14.4	84.7	17	6	128855	128855 Sequence 11
6	14.4	84.7	17	6	179225	179225 Sequence 11
7	14.4	84.7	345	6	AR070288	AR070288 Sequence
8	14.4	84.7	345	6	AR070289	AR070289 Sequence
9	14.4	84.7	345	6	AR085747	AR085747 Sequence
10	14.4	84.7	345	6	AR085748	AR085748 Sequence
11	14.4	84.7	345	6	128856	128856 Sequence 12
12	14.4	84.7	345	6	128857	128857 Sequence 13
13	14.4	84.7	345	6	179226	179226 Sequence 12
14	14.4	84.7	345	6	179227	179227 Sequence 13
15	14.4	84.7	453	9	HS1L15MR	238000 H.sapiens m
16	14.4	84.7	486	9	HS1L15	Y09908 H.sapiens m
17	14.4	84.7	489	4	AF108148	AF108148 Felis cat
18	14.4	84.7	489	6	AR004267	AR004267 Sequence
19	14.4	84.7	489	6	AR004268	AR004268 Sequence
20	14.4	84.7	489	6	AR024348	AR024348 Sequence
21	14.4	84.7	489	6	AR024349	AR024349 Sequence
22	14.4	84.7	489	6	AR070281	AR070281 Sequence
23	14.4	84.7	489	6	AR070282	AR070282 Sequence
24	14.4	84.7	489	6	AR085740	AR085740 Sequence
25	14.4	84.7	489	6	AR085741	AR085741 Sequence
26	14.4	84.7	489	6	AR094649	AR094649 Sequence
27	14.4	84.7	489	6	AR094650	AR094650 Sequence
28	14.4	84.7	489	6	AR122045	AR122045 Sequence
29	14.4	84.7	489	6	AR122046	AR122046 Sequence
30	14.4	84.7	489	6	AR122867	AR122867 Sequence
31	14.4	84.7	489	6	AR122868	AR122868 Sequence
32	14.4	84.7	489	6	AR125104	AR125104 Sequence
33	14.4	84.7	489	6	AR125105	AR125105 Sequence
34	14.4	84.7	489	6	AX006785	AX006785 Sequence
35	14.4	84.7	489	6	AX006786	AX006786 Sequence
36	14.4	84.7	489	6	AX320242	AX320242 Sequence
37	14.4	84.7	489	6	AX320244	AX320244 Sequence
38	14.4	84.7	489	6	BD008811	BD008811 Antagonis
39	14.4	84.7	489	6	BD008812	BD008812 Antagonis
40	14.4	84.7	489	6	125782	125782 Sequence 1
41	14.4	84.7	489	6	125783	125783 Sequence 4
42	14.4	84.7	489	6	128849	128849 Sequence 1
43	14.4	84.7	489	6	128850	128850 Sequence 4
44	14.4	84.7	489	6	162692	162692 Sequence 1
45	14.4	84.7	489	6	179219	179219 Sequence 1

## ALIGNMENTS

RESULT 1  
AR004273 AR004273 Sequence 11 from patent US 5747024. 17 bp DNA linear PAT 04-DEC-1998

LOCUS AR004273  
DEFINITION AR004273  
ACCESSION AR004273  
VERSION AR004273.1 GI:3965152  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Grabstein,K.H. and Widmer,M.B.  
TITLE Vaccine adjuvant comprising Interleukin-15  
JOURNAL Patent: US 5747024-A 11 05-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..17  
BASE COUNT 2 a 4 c 1 g 5 t 5 others

Query Match 84.7%: Score 14.4: DB 6: Length 17;  
Best Local Similarity 100.0%: Pred. No. 7.6e+02;





Wed Jun 19 09:13:58 2002

us-09-724-841-10.rn1

Page 7

Search completed: June 19, 2002, 02:22:12  
Job time: 5420 sec

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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,214  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,498  
FILING DATE: 04-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UTSD:450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4008 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-726-214-3

Query Match 81.2%; Score 13.8; DB 3; Length 4008;  
Best Local Similarity 70.6%; Pred. No. 27;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTGCAVTCNGTGTGA 17  
11:11 11:11 11:11  
DB 2780 ACATCTGACTGTGTGA 2764

RESULT 14  
PCT-US95-11808-5/c  
Sequence 5, Application PC/TUS9511808  
GENERAL INFORMATION:  
APPLICANT: Iyengar, Srinivas Ravi V.  
TITLE OF INVENTION: MUTANT ACTIVATED GALPHA AND  
TITLE OF INVENTION: ADENYLYL  
TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brumbaugh, Graves, Donohue and  
ADDRESS: Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.  
ZIP: 10112-0228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/11808  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/307,896  
FILING DATE: 16-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Richard S.  
REGISTRATION NUMBER: 26,154  
REFERENCE/DOCKET NUMBER: 29970 165/28755  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 408-2500  
TELEFAX: (212) 765-2519  
TELEX: 650 6111063  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4008 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
PCT-US95-11808-5

Query Match 81.2%; Score 13.8; DB 5; Length 4008;  
Best Local Similarity 70.6%; Pred. No. 27;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTGCAVTCNGTGTGA 17  
11:11 11:11 11:11  
DB 2780 ACATCTGACTGTGTGA 2764

RESULT 15  
US-08-860-368B-18  
Sequence 18, Application US/08860368B  
Patent No. 6002072  
GENERAL INFORMATION:  
APPLICANT: McMaster, Russell J.  
APPLICANT: Boeshore, Maury L.  
APPLICANT: Tricoli, David M.  
APPLICANT: Reynolds, John F.  
APPLICANT: Carney, Kim J.  
TITLE OF INVENTION: Papaya Ringspot Virus Coat Protein Gene  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rockey, Milnamow & Katz, Ltd.  
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,  
CITY: Chicago  
STATE: IL  
COUNTRY: U.S.A.  
ZIP: 60601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,368B  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Mueller, Lisa L.  
REGISTRATION NUMBER: 38,978  
REFERENCE/DOCKET NUMBER: SVS3801P01810S  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-616-5400  
TELEFAX: 312-616-5460  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 906 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: DNA (genomic)  
US-08-860-368B-18

Query Match 75.3%; Score 12.8; DB 3; Length 906;  
Best Local Similarity 68.8%; Pred. No. 87;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 CRTGCAVTCNGTGTGA 17  
11:11 11:11 11:11  
DB 258 CATCTGATTCAGTATA 273

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0Y      1 ACRTCTGAYTCNGSTR 17
         ||:| | | :| | | :| |
Db      1043 ACATCTGACTCTGTGT 1027

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```

RESULT 10
US-08-307-896-6/c
: Sequence 6, Application us/08307896C
: Patent No. 6034071
: GENERAL INFORMATION:
: APPLICANT: Iyengar, Shilvas Rayl
: TITLE OF INVENTION: NOTAN ACTIVATED GSALL
: TITLE OF INVENTION: CCCLASE 2 FOR USE AS 1
: FILE REFERENCE: 29770
: CURRENT APPLICATION NUMBER: US/08/307,896C
: CURRENT FILING DATE: 1994-09-16
: NUMBER OF SEQ ID NOS: 94
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 6
: LENGTH: 2092
: TYPE: DNA
: ORGANISM: Homo sapiens
US-08-307-896-6

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Query Match	81.2%	Score 13.8	DB 3	Length 2092
Best Local Similarity	70.6%	Pred. No. 25		
Matches 12; Conservative	3	Mismatches 2	Indels 0	Gaps 0

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QY      1 ACRTGNGAYTCNGTRTA 17
      ||:|| ||:|| ||:||
Db      869 ACGTCGGATTCTGTATA 853

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RESULT 11  
PCT-US95-11808-6/C  
Sequence 6, Application PC/TUS9511808  
GENERAL INFORMATION:  
APPLICANT: Iyengar, Srinivas Ravi V.  
TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND  
TITLE OF INVENTION: ADENITYL  
TITLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brumbaugh, Graves, Donohue and  
ADDRESSEE: Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: U.S.  
ZIP: 10112-0228  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/11808  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/307,896  
FILING DATE: 16-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Richard S.  
REGISTRATION NUMBER: 26,154  
REFERENCE/DOCKET NUMBER: 29970 165/28755  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 408-2500  
TELEFAX: (212) 765-2519  
TELEX: 650 6111063  
INFORMATION FOR SEQ ID NOS: 6:  
SEQUENCE CHARACTERISTICS:

```

:
: LENGTH: 2092 base pairs
: type: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 1..2092
:   OTHER INFORMATION: /product= "adenylyl cyclase"
:   OTHER INFORMATION: 2
:   OTHER INFORMATION: (partial)"
:
: DCT-US95-11808-6

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Query Match	81.2%	Score 13.8;	DB 5;	Length 2092;
Best Local Similarity	70.6%	Pred. No. 25;		
Matches 12; Conservative	3;	Mismatches 2;	Indels 0;	Gaps 0;

```
QY      1 ACRTGNGAYTCNGTRTA 17
          ||:|| ||:|| ||:||
Db      869 ACGTCGATTCTGTATA 853
```

```

RESULT 12
US-08-307-896-5/c
: Sequence 5, Application US/08307896C
: Patent No. 6034071
GENERAL INFORMATION:
APPLICANT: Iyengar, Srinivas Ravi
TITLE OF INVENTION: MUTANT ACTIVATED GALPHEA AND ADENITYL
: FILE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
: FILE REFERENCE: 293770
CURRENT APPLICATION NUMBER: US/08/307,896C
CURRENT FILING DATE: 1994-09-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 4008
TYPE: DNA
ORGANISM: Rattus norvegicus
: US-08-307-896-5

```

Query Match	81.2%	Score 13.8	DB 3	Length 4008
Best Local Similarity	70.6%	Pred. No. 2		
Matches 12; Conservative	3	Mismatches	2	Gaps 0

QY 1 ACRTCNGAYTCNGTRTA 17  
11:1111111111  
Db 2780 ACATCTGACTCTGTGTA 2764

RESULT 13  
US-08-726-214-3/C  
Sequence 3, Application US/08726214  
Patent No. 6107076  
GENERAL INFORMATION:  
APPLICANT: Tang, Wei-Jen  
APPLICANT: Gilman, Alfred G.  
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE  
TITLE OF INVENTION: AND USES THEREFOR  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/189,193  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-189-193-10

Query Match 81.2%; Score 13.8; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGAYTCNGTRTA 17  
DB 1 ACRTGAYTCNGTRTA 17

RESULT 8  
PCT-US94-03793-10  
Sequence 10, Application PC/TUS9403793  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: Interleukin-15  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/03793  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Launer, Charlene  
REGISTRATION NUMBER: 33,035

REFERENCE/DOCKET NUMBER: 2811  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
PCT-US94-03793-10

Query Match 81.2%; Score 13.8; DB 5; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGAYTCNGTRTA 17  
DB 1 ACRTGAYTCNGTRTA 17

RESULT 9  
US-08-726-214-17/C  
Sequence 17, Application US/08726214  
Patent No. 6107076  
GENERAL INFORMATION:  
APPLICANT: Tang, Wei-Jen  
APPLICANT: Gilman, Alfred G.  
TITLE OF INVENTION: SOLUBLE MAMMALIAN ADENYLYL CYCLASE  
TITLE OF INVENTION: AND USES THEREFOR  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,214  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/005,498  
FILING DATE: 04-OCT-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UTSID:450  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1652 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-726-214-17

Query Match 81.2%; Score 13.8; DB 3; Length 1652;  
Best Local Similarity 70.6%; Pred. No. 24;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

REFERENCE/DOCKET NUMBER: 2811  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOHETICAL: NO  
ANTI-SENSE: YES  
US-08-504-042-10

Query Match 81.2%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGNGAYTCNGTCTTA 17  
Db 1 ACRTGNGAYTCNGTCTTA 17

RESULT 5  
US-08-725-969-10  
Sequence 10, Application US/08725969  
Patent No. 5892001  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/725,969  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-725-969-10

Query Match 81.2%; Score 13.8; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGNGAYTCNGTCTTA 17  
Db 1 ACRTGNGAYTCNGTCTTA 17

RESULT 6  
US-08-794-524-10  
Sequence 10, Application US/08794524  
Patent No. 5985262  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/794,524  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-794-524-10

Query Match 81.2%; Score 13.8; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGNGAYTCNGTCTTA 17  
Db 1 ACRTGNGAYTCNGTCTTA 17

RESULT 7  
US-09-189-193-10  
Sequence 10, Application US/09189193  
Patent No. 6184359  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15

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Db 1 ACRTGNGAYTCNGTRTA 17
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RESULT 2  
 US-08-393-305-10  
 : Sequence 10, Application US/08393305  
 : Patent No. 5574138  
 : GENERAL INFORMATION:  
 : APPLICANT: Grabstein, Kenneth  
 : APPLICANT: Anderson, Dirk  
 : APPLICANT: Eisenman, June  
 : APPLICANT: Fung, Victor  
 : APPLICANT: Rauch, Charles  
 : TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR  
 : NUMBER OF SEQUENCES: 15  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Seed and Berry  
 : STREET: 6300 Columbia Center, 701 Fifth Avenue  
 : CITY: Seattle  
 : STATE: Washington  
 : COUNTRY: USA  
 : ZIP: 98104  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentL Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/393, 305  
 : FILING DATE: 22-FEB-1995  
 : CLASSIFICATION: 424  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: McMasters, David D.  
 : REGISTRATION NUMBER: 33, 963  
 : REFERENCE/DOCKET NUMBER: 480052, 409C2  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 206-622-4900  
 : INFORMATION FOR SEQ ID NO: 10:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 17 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear

RESULT 3  
US-08-726-817-10  
Sequence 10, Application US/08726817  
Patent No. 5707616  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPIITHELUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle

STATE: Washington  
COUNTRY: USA  
Zip: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,817  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: McMaisters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-726-817-10

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 02:22:11 ; Search time 66.01 seconds  
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Title: US-09-724-841-10

Sequence: 1 ACRTGNGAYTCNGTRTA 17

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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	13.8	81.2	17	US-08-393-305-10	Sequence 10, Appl
3	13.8	81.2	17	US-08-726-817-10	Sequence 10, Appl
4	13.8	81.2	17	US-08-504-042-10	Sequence 10, Appl
5	13.8	81.2	17	US-08-725-969-10	Sequence 10, Appl
6	13.8	81.2	17	US-08-794-524-10	Sequence 10, Appl
7	13.8	81.2	17	US-09-189-193-10	Sequence 10, Appl
8	13.8	81.2	17	PCT-US94-03793-10	Sequence 10, Appl
9	13.8	81.2	1652	US-08-726-214-17	Sequence 10, Appl
10	13.8	81.2	2092	US-08-307-896-6	Sequence 6, Appl
11	13.8	81.2	2092	PCT-US95-11808-6	Sequence 6, Appl
12	13.8	81.2	4008	US-08-307-896-5	Sequence 5, Appl
13	13.8	81.2	4008	US-08-726-214-3	Sequence 3, Appl
14	13.8	81.2	4008	PCT-US95-11808-5	Sequence 5, Appl
15	12.8	75.3	906	US-08-860-368B-18	Sequence 18, Appl
16	12.8	75.3	1588	US-08-865-486A-10	Sequence 10, Appl
17	12.8	75.3	1588	US-08-880-342-10	Sequence 10, Appl
18	12.2	71.8	1327	US-08-507-431-3	Sequence 3, Appl
19	12.2	71.8	1327	US-08-700-546-1	Sequence 1, Appl
20	12.2	71.8	1327	US-08-902-655A-3	Sequence 3, Appl
21	12.2	71.8	1327	US-09-116-622-3	Sequence 3, Appl
22	12.2	71.8	1327	US-09-219-277-3	Sequence 3, Appl
23	12.2	71.8	1327	US-09-599-661-3	Sequence 3, Appl
24	12.2	71.8	4291	US-08-417-210A-81	Sequence 81, Appl
25	12.2	71.8	5199	US-08-726-214-13	Sequence 13, Appl
26	12.2	71.8	17710	US-08-976-259-70	Sequence 70, Appl
27	11.8	69.4	115	US-07-920-281C-4	Sequence 4, Appl

#### ALIGNMENTS

C	28	11.8	69.4	115	4	US-08-466-277-4	Sequence 4, Appl
	29	11.8	69.4	1449	4	US-08-858-207A-68	Sequence 68, Appl
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	31	11.8	69.4	1876	3	US-08-700-636-7	Sequence 7, Appl
	32	11.8	69.4	1876	3	US-08-467-574-7	Sequence 7, Appl
	33	11.8	69.4	1876	4	US-09-217-345-7	Sequence 7, Appl
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	35	11.8	69.4	1929	5	PCT-US91-07635-3	Sequence 3, Appl
	36	11.8	69.4	2208	5	PCT-US95-08493-1	Sequence 1, Appl
	37	11.8	69.4	2336	4	US-08-796-101-47	Sequence 47, Appl
	38	11.8	69.4	2580	5	PCT-US95-08493-18	Sequence 18, Appl
	39	11.8	69.4	2604	5	PCT-US95-08493-20	Sequence 20, Appl
	40	11.8	69.4	2610	1	US-08-374-834-17	Sequence 17, Appl
	41	11.8	69.4	2610	1	US-08-644-271-28	Sequence 28, Appl
	42	11.8	69.4	2869	1	US-08-374-834-2	Sequence 2, Appl
	43	11.8	69.4	3398	5	US-08-644-271-2	Sequence 2, Appl
	44	11.8	69.4	3398	5	PCT-US95-08493-12	Sequence 12, Appl
	45	11.8	69.4	3872	2	US-08-331-081B-4	Sequence 4, Appl

#### RESULT 1

US-08-031-399-10  
Sequence 10, Application US/08031399  
Patent No. 5552303  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: Epithelium-derived T-cell factor  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/031,399  
FILING DATE: 19930308  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Launer, Charlene  
REGISTRATION NUMBER: 33,035  
REFERENCE/DOCKET NUMBER: 2811  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-031-399-10

Query Match 81.2%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





## COMMENT

Vector: pBluescript II KS  
V\_type: phagemid  
PRIMER: KS  
DESCR:

One pass dye-terminator sequencing of cosmid cloned genomic sequence.

## FEATURES

Location/Qualifiers  
1..583

/organism="Takifugu rubripes"  
/db\_xref="taxon:31033"  
/clone\_1lb="cosmid 103j15"  
/clone="103j15a5"

BASE COUNT 135 a 122 c 134 g 184 t 8 others  
ORIGIN

Job time: 7366 sec

## Query Match

Best Local Similarity 81.2%; Score 13.8; DB 12; Length 583;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTGCAATTCGCTGA 17  
11:11 11:11 11:11

DB 406 ACCTCAGATTCGGTGA 390

## RESULT 15

FR0039660/c

LOCUS Fugu rubripes GSS sequence, clone 103j15a64, genomic survey

DEFINITION

sequence.

ACCESSION AL127155

VERSION GSS: genome survey sequence.

KEYWORDS Takifugu rubripes.

SOURCE Takifugu rubripes

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Takifugu.

1 (bases 1 to 597)

Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,

Umranta,Y., Williams,G. and Brenner,S.

Direct Submission

Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource

Centre, Hinxton, Cambridge, CB10 1SB. UK Email:

biohelp@hgm.mrc.ac.uk

Vector: pBluescript II KS

V\_type: phagemid

PRIMER: KS

DESCR:  
One pass dye-terminator sequencing of cosmid cloned genomic sequence.

Location/Qualifiers

1..597

/organism="Takifugu rubripes"

/db\_xref="taxon:31033"

/clone\_1lb="cosmid 103j15"

/clone="103j15a64"

BASE COUNT 138 a 129 c 136 g 176 t 18 others  
ORIGIN

## Query Match

Best Local Similarity 81.2%; Score 13.8; DB 12; Length 597;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTGCAATTCGCTGA 17  
11:11 11:11 11:11

DB 405 ACCTCAGATTCGGTGA 389

Search completed: June 19, 2002, 02:15:53

RESULT 12  
AA034789/c  
LOCUS  
DEFINITION  
AA034789 556 bp mRNA linear EST 23-AUG-1996  
m153605.r1 Soares mouse embryo Nbm13.5 14.5 Mus musculus cDNA  
clone IMAGE:467241 5' similar to gb:U1993 ADENYLATE CYCLASE, TYPE  
II (HUMAN); gb:U12919 Mus musculus adenyllyl cyclase type VII mRNA,  
complete (MOUSE); mRNA sequence.

ACCESSION  
AA034789  
VERSION  
AA034789.1 GI:1506671  
KEYWORDS  
EST.  
SOURCE  
house mouse.  
ORGANISM  
Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 556)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
COMMENT  
Contact: Maria M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
MGI:281057  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 411.  
Location/Qualifiers  
1..556  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_image="467241"  
/clone\_lib="Soares mouse embryo NBM13.5 14.5"  
/sex="unknown"  
/tissue\_type="embryo"  
/dev\_stage="13.5-14.5dpc total fetus"  
/lab\_host="DH10B"  
/note="Vector: p7773D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5',  
TGTTCACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTT  
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2  
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne  
State Univ., from 2 1; double-stranded cDNA was ligated to  
Eco RI adaptors (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of the modified  
p7773 vector. Library went through one round of  
normalization, and was constructed by Bento Soares and  
M.Petina Bonaldo."

BASE COUNT 146 a 131 c 146 g 133 t  
ORIGIN

Query Match 81.2%; Score 13.8; DB 9; Length 556;  
Best Local Similarity 70.6%; Pred. No. 1.6e+03;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTCNGAYTCGTCTA 17  
||:||||:||||:||||  
Db 298 ACATCTGACTCGTCTA 282

RESULT 13  
BI341029/c  
LOCUS  
BI341029 573 bp mRNA linear EST 30-JUL-2001

DEFINITION  
368222 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.  
ACCESSION  
BI341029  
VERSION  
BI341029.1 GI:15034318  
KEYWORDS  
EST.  
SOURCE  
pig.  
ORGANISM  
Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
REFERENCE  
1 (bases 1 to 573)  
Stohrenkrug,S.C., Fireking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,  
Fahnenkrug,S.C., Fireking,B.A., Rohrer,G.A., Smith,T.P.L.,  
and Keeler,J.W.  
Design and use of two pooled tissue normalized cDNA libraries for  
EST discovery in swine  
Unpublished (2000)  
COMMENT  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt-trimmed with phred  
v0.980904.e. Vector identified by cross-match with the -minscore 18  
and -mismatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTCAGTACAGCAGC  
Plate: 107 row: N column: 5  
Seq primer: ATTTCAGTACCTATGAG.  
Location/Qualifiers  
1..573  
/organism="Sus scrofa"  
/db\_xref="taxon:9823"  
/clone\_lib="MARC 2P1G"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled tissue from testis, ovary,  
endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT 140 a 152 c 161 g 119 t  
ORIGIN

Query Match 81.2%; Score 13.8; DB 10; Length 573;  
Best Local Similarity 70.6%; Pred. No. 1.6e+03;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTCNGAYTCGTCTA 17  
||:||||:||||:||||  
Db 138 ACGTCTGATTCGTCTA 122

RESULT 14  
FR0039639/c  
LOCUS  
DEFINITION  
FR0039639 583 bp DNA linear GSS 22-OCT-1999  
Fugu rubripes GSS sequence, clone 103J15aE5, genomic survey  
sequence.  
ACCESSION  
AL127134  
VERSION  
AL127134.1 GI:6108749  
KEYWORDS  
GSS: genome survey sequence.  
SOURCE  
Takifugu rubripes.  
ORGANISM  
Takifugu rubripes.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Takifugu.  
1 (bases 1 to 583)  
REFERENCE  
Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,  
Umranta,Y., Williams,G. and Brenner,S.  
Direct Submission  
Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource  
Centre, Hinxton, Cambridge, CB10 1SB. UK Email:  
biohelp@hgm.mrc.ac.uk

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LLAM8441 row: c column: 16

High quality sequence stop: 500.

Location/Qualifiers

1. 502

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:3455175"

/clone\_lib="NIH\_MGC\_12"

/tissue\_type="cervical carcinoma cell line"

/lab\_host="DH10B"

/note="Organ: Cervix; Vector: PCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.4 kb. Library prepared by Life

Technologies."

BASE COUNT 144 a 73 c 87 g 198 t

ORIGIN

Query Match

Best Local Similarity 70.6%; Score 13.8; DB 10; Length 502;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGCAATTCGCTGTA 17

Db 33 ACATCCGATTCGTGTA 49

RESULT 10  
FR0039629 518 bp DNA linear GSS 22-OCT-1999

LOCUS Fugu rubripes GSS sequence, clone 103J15aF1, genomic survey

DEFINITION sequence.

ACCESSION AL127124.1 GI:6108739

VERSION AL127124.1 GI:6108739

KEYWORDS GSS; genome survey sequence.

SOURCE Takifugu rubripes.

ORGANISM Takifugu rubripes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes; Tetraodontidae; Takifugu.

1 (bases 1 to 518)

Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y.J.K.,

Umanita,Y., Williams,G. and Brenner,S.

Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource

Centre, Hinxton, Cambridge, CB10 1SB. UK Email:

biohelip@hmp.mrc.ac.uk

Vector: pBluescript II KS

V\_type: phagemid

PRIMER: KS

DESCR: One pass dye-terminator sequencing of cosmid cloned genomic

sequence.

Location/Qualifiers

1. 518

/organism="Takifugu rubripes"

/db\_xref="taxon:31033"

/clone\_lib="cosmid 103J15"

/clone="103J15aF1"

BASE COUNT 148 a 122 c 116 g 126 t 6 others

ORIGIN

Query Match 81.2%; Score 13.8; DB 12; Length 518;

Best Local Similarity 70.6%; Pred. No. 1.5e+03;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGCAATTCGCTGTA 17

11:11 11:11 11:11

Db 415 ACCTCAGATTCGCTGTA 431

RESULT 11

AW766896

LOCUS

DEFINITION

AW766896 528 bp mRNA linear EST 16-FEB-2001

da6d11.y1 Harland stage 19-23 Xenopus laevis cDNA clone

IMAGE:3199413 5' similar to TR:097754 097754 TITIN ;, mRNA

sequence.

AW766896.1 GI:7698968

VERSION AW766896

KEYWORDS EST.

SOURCE African clawed frog.

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

Xenopodinae; Xenopus.

1 (bases 1 to 528)

Clifton,S., Johnson,S.L., Blumberg,B., Song,D., Hillier,L., Pape,D.

, Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person

, B., Gibbons,M., Harvey,N., Rittler,E., Jackson,Y., McCann,R.,

Waterston,R. and Wilson,R. 1999

Unpublished (1999)

Contact: Sandy Clifton, Ph.D.

Washu Xenopus EST project, 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Library constructed by R. Harland, PhD (University of California,

Berkeley)

DNA sequencing by: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available

through the I.M.A.G.E. Consortium/LINL at:

image.llnl.gov/image/html/resources.shtml

Seq primer: -40RP from GIBCO

High quality sequence stop: 489.

Location/Qualifiers

1. 528

/organism="Xenopus laevis"

/db\_xref="taxon:8355"

/clone="IMAGE:3199413"

/clone\_lib="Harland stage 19-23"

/tissue\_type="neurala"

/dev\_stage="stage 19-23"

/lab\_host="DH10B (phage-resistant)"

/note="Vector: pCS107 (custom); Site\_1: NotI; Site\_2: SalI

; cDNA made by oligo-dT priming. Library constructed by

Dr. Francesca Mariani in the laboratory of R. Harland,

Ph.D. (University of California, Berkeley). References:

XBF-2 is a transcriptional repressor that converts

ectoderm into neural tissue. Mariani, FV, Harland, RM,

Development. 1998 Dec;125(24):5019-31. PMID: 9811566; UI:

99030283; Use of large-scale expression cloning screens in

the xenopus laevis tadpole to identify gene function.

Gramer TC, Liu KJ, Mariani FV, Harland RM, Dev Biol.

2000 Dec 15;228(2):197-210. PMID: 1112324; UI: 20564075;

Note: This is a Xenopus Gene Collection (XGC) library."

BASE COUNT 188 a 100 c 114 g 125 t 1 others

ORIGIN

Query Match 81.2%; Score 13.8; DB 9; Length 528;

Best Local Similarity 70.6%; Pred. No. 1.5e+03;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGCAATTCGCTGTA 17

Db 108 ACATCAGATTCGCTGTA 124

KEYWORDS EST.  
SOURCE African clawed frog.  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
Xenopodinae; Xenopus.  
REFERENCE 1 (bases 1 to 472)  
AUTHORS Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Haller,L., Pape,D.,  
Martin,J., Wylie,T., Underwood,K., Thaising,B., Bowers,Y., Person  
,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,  
Waterston,R. and Wilson,R.  
TITLE Washu Xenopus EST project, 1999  
JOURNAL Unpublished (1999)  
COMMENT Contact: Sandy Clifton, Ph.D.  
Washu Xenopus EST project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Library constructed by Bento Soares and M. Fatima Bonaldo  
(University of Iowa). DNA Sequencing by: Washington University  
Genome Sequencing Center  
Clone distribution: Xenopus clones from this library are available  
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov  
Seq primer: -40UP from Gibco  
High quality sequence stop: 450.  
FEATURES  
Source  
1..472  
Location/Qualifiers  
/organism="Xenopus laevis"  
/db\_xref="taxon:8355"  
/clone="IMAGE:4783632"  
/clone.lib="Blackshear/Soares normalized Xenopus egg  
library"  
/sex="female"  
/tissue\_type="unfertilized egg"  
/cell\_type="unfertilized egg"  
/dev\_stage="unfertilized egg"  
/lab\_host="DH10B"  
/note="Vector: pT73-Pac; Site.1: EcoRI; Site.2: NotI;  
POLYA-selected mRNA was prepared from unfertilized Xenopus  
laevis eggs. The library was constructed in the vector  
pT73-Pac as described in Bonaldo, M.F., Lennon, G. and  
Soares, M.B. 'Normalization and subtraction: two  
approaches to facilitate gene discovery', Genome Research  
6:791-806, 1996. The first strand synthesis used a  
NotI-dT18 primer: double stranded cDNAs were ligated to  
EcoRI adapters, digested with NotI, and directionally  
cloned into the NotI and EcoRI-digested pT73-Pac vector.  
The library contained approximately 7.2 x 10<sup>5</sup>  
recombinants, with average insert sizes of 1-1.5 kb."  
BASE COUNT 109 a 110 c 135 g 118 t  
ORIGIN  
Query Match 81.2%; Score 13.8; DB 10; Length 472;  
Best Local Similarity 70.6%; Pred. No. 1.5e+03;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ACRTCGATTCNGTCTTA 17  
11:11 11:11 11:11  
DB 162 ACATCTGATTCGTCTGTA 146  
RESULT 8  
LOCUS AI380969 478 bp mRNA linear EST 30-MAR-1999  
DEFINITION tg18d12.x1 NCI-CCAP-CL11 Homo sapiens cDNA clone IMAGE:2109143 3',  
mRNA sequence.  
ACCESSION AI380969  
VERSION AI380969.1 GI:4190822  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 478)  
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-ri@mail.nih.gov  
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,  
M.D., Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. consortium/LLNL at:  
www-bio.llnl.gov/db/rrp/image/image.html  
Insert length: 444 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 466.  
FEATURES  
Source  
1..478  
Location/Qualifiers  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2109143"  
/clone.lib="NCI-CCAP-CL11"  
/tissue\_type="B-cell, chronic lymphocytic leukemia"  
/lab\_host="DH10B"  
/note="Vector: pT73D-Pac (Pharmacia) with a modified  
polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer (5'  
TCTTCCATCTGAGATGGAGCGCCGACATGCGTCTTTTCTTTTCTTTTCTTTT  
T 3'); double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT73 vector.  
Library is normalized, and was constructed by Bento  
Soares and M. Fatima Bonaldo."  
BASE COUNT 146 a 102 c 80 g 149 t 1 others  
ORIGIN  
Query Match 81.2%; Score 13.8; DB 9; Length 478;  
Best Local Similarity 70.6%; Pred. No. 1.5e+03;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ACRTCGATTCNGTCTTA 17  
11:11 11:11 11:11  
DB 106 ACCTCTGATTCGTCTGTA 122  
RESULT 9  
LOCUS BE543117 502 bp mRNA linear EST 09-AUG-2000  
DEFINITION 601069058F1 NIH-MGC\_12 Homo sapiens cDNA clone IMAGE:3455175 5',  
mRNA sequence.  
ACCESSION BE543117  
VERSION BE543117.1 GI:97711762  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-ri@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.

FEATURES	Location/Qualifiers
SOURCE	1..416
	/organism="Xenopus laevis"
	/db_xref="taxon:8355"
	/clone="XL042d11"
	/library="NIBB Mochi1 normalized Xenopus neurula library"
	/tissue_type="whole embryo"
	/dev_stage="stage 15"
BASE COUNT	91 a 96 c 128 g 100 t 1 others
ORIGIN	
Query Match	81.2%; Score 13.8; DB 10; Length 416;
Best Local Similarity	70.6%; Pred. No. 1.4e+03;
Matches 12: Conservative	3; Mismatches 2; Indels 0; Gaps 0;
QY	1 ACRTCGAYTCNGTCTTA 17
DB	125 ACATCTGATCTCTGTGA 109
RESULT	5
B53166	419 bp DNA linear GSS 20-JUN-1998
LOCUS	CIT-HSP-2009B4.TR CIT-HSP Homo sapiens genomic clone 2009B4, DNA
DEFINITION	sequence.
ACCESSION	B53166
VERSION	B53166.1 GI:2607500
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 419)
AUTHORS	Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden
	,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M.
	and Venter,J.C.
TITLE	Use of a random BAC End Sequence Database for Sequence-Ready Map
	Building
JOURNAL	Unpublished (1997)
COMMENT	Other_GSSs: CIT-HSP-2009B4.TF
	Contact: Mark Adams
	Department of Eukaryotic Genomics
	The Institute for Genomic Research
	9712 Medical Center Dr., Rockville, MD 20850, USA
	Tel: 301 838 0200
	Fax: 301 838 0208
	Email: mdamads@tigr.org
	Clones are available from Research Genetics (Info@resgen.com). BAC
	end search page:
	http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
	Seq primer: M13 Reverse
	Class: BAC ends.
FEATURES	Location/Qualifiers
SOURCE	1..419
	/organism="Homo sapiens"
	/db_xref="GDB:7040670"
	/db_xref="taxon:9606"
	/clone="2009B4"
	/clone_1lb="CIT-HSP"
	/sex="Male"
	/cell_type="Sperm"
	/note="Vector: pBeloBAC11; site_1: HindIII; site_2:
	HindIII"
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ORIGIN	
Query Match	81.2%; Score 13.8; DB 12; Length 419;
Best Local Similarity	70.6%; Pred. No. 1.4e+03;
Matches 12: Conservative	3; Mismatches 2; Indels 0; Gaps 0;

QY	1	ACRTGCAVTCNGTRTA	17	
Db	205	ACATCGATTCTGTATA	221	
RESULT	6			
LOCUS	BG017447/c			
DEFINITION	BG017447	470 bp	mRNA	linear
	de6b12.x1 Kirschner embryo St10 14 Xenopus laevis cDNA clone			
	IMAGE:516263 3' similar to SW:SRB7_HUMAN Q13503 RNA POLYMERASE II			
ACCESSION	BG017447			
VERSION	1			
KEYWORDS	EST			
SOURCE	African clawed frog.			
ORGANISM	Xenopus laevis			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;			
	Xenopus; Xenopus.			
REFERENCE	1 (bases 1 to 470)			
AUTHORS	Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Miller,L., Page,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person, B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.			
	Washu Xenopus EST project, 1999			
TITLE	Unpublished (1999)			
JOURNAL	Contact: Sandy Clifton, Ph.D.			
COMMENT	Washu Xenopus EST project, 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.edu Library constructed by M. Kirschner (Harvard Medical School). DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LNL at: info@image.llnl.gov Seq primer: -400P from Glenco High quality sequence stop: 315. Location/Qualifiers 1..470 /organism="Xenopus laevis" /db_xref="taxon:8355" /clone="IMAGE:3516263" /clone_id="Kirschner embryo St10 14" /tissue_type="Pooled embryos (stage 10-14)" /lab_host="DH10B (phage-resistant)" /note="Vector: pCS2+; Site.1: NotI; Site.2: SalI; Size-selected for average insert size 1.2 kb. Library was constructed and donated by M. Kirschner (Harvard Medical School)."			
BASE COUNT	110 a	95 c	130 g	135 t
ORIGIN				
Query Match		81.2%	Score 13.8	DB 10;
Best Local Similarity		70.6%	Pred. No. 1.5e+03;	Length 470;
Matches 12; Conservative		3;	Mismatches 2;	Indels 0;
Gaps		0;		
QY	1	ACRTGCAVTCNGTRTA	17	
Db	166	ACATCGATTCTGTATA	150	
RESULT	7			
LOCUS	BM191868/c			
DEFINITION	BM191868	472 bp	mRNA	linear
	dag37f01.x3 Blackshear/Soares normalized Xenopus egg library			
	Xenopus laevis cDNA clone IMAGE:4783632 3' similar to SW:SRB7_HUMAN			
	Q13503 RNA POLYMERASE II HOLOENZYME COMPONENT SRB7 ;, mRNA			
ACCESSION	BM191868			
VERSION	1			
	GI:17527831			

Indels 0; Gaps 0;

LOCUS	352 bp	mRNA	linear	EST 09-OCT-2000
DEFINITION	ADB Homo sapiens CDNA clone ADBBR04 5',			mRNA sequence.
ACCESSION	AV705097			
AV705097				

human.

REFERENCE  
AUTHORS  
1 (bases 1 to 352)  
Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao

Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z., and Han, Z.

JOURNAL  
unpublished (2000)  
COMMENT  
Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai

**FEATURES**

This clone is available at CHGC in Shanghai

Location/Qualifiers

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/organism="Homo sapiens"  
/db_xref="taxon:9606"
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ORIGIN				

Query Match	81.2%;	Score 13.8;	DB 9;	Length 352
Best Local Similarity	70.6%;	Pred. No. 1.3e+03;		
Matches 12;	Conservative 3;	Mismatches 2;	Indels	

QY	1	ACRTCNGAYTCNGTRTA	17
		:      :      :	
Db	178	ACGTCGGATTCTGTATA	162

DEFINITION	405 bp	linear	EST 18-JAN-2001
DEFINITION	CM4-TN0146-301000-381-e02	TN0146	Homo sapiens cDNA, mRNA sequence.
ACCESSION	BF887255		

KEYWORDS	EST.
SOURCE	human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
1 / Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AMORIM  
DUAS NEVO, E., Garcia Correia, R., Verjovski-Almeida, S., Briones, M. R.,  
Nagai, M. A., da Silva, W. Jr., Zago, M. J., Bordin, S., Costa, F. F.,  
Goldman, G. H., Carvalho, A. F., Matsuikuma, A., Baia, G. S., Simpson, D. H.,

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G.

Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP  
Brazil

Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)  
This sequence was derived from the EMBL/GenBank/CC-0

(<http://www.ludwig.org.br/scripts/gethtml2.pl?P1=Cm4&t2=Cm4-TN01301000-381-e02&t3=2000-10-30&t4=1>)

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High quality sequence stop: 405.

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%>% summarise(n =  
862)
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/clone_lib="jN0146"
/dev_stage="Adult"
/note="Organ: testis normal; vector: env18; site: 1; sex:

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size=2: smad1, a mini-librady was made by cloning product  
 derived from ORESTES PCR (U.S. Letters Patent applicat  
 No. 196,716 - Ludwig Institute for Cancer Research)

tissue mRNA and cDNA amplification were performed under low stringency conditions."

# ORIGIN

Query match	81.2%	Score 13.8;	DB 10;	Length 405;
Best Local Similarity	70.6%;	Pred. NO. 1.4e+03;		
Matches 12; Conservative	3; Mismatches	2; Indels	0; Gaps	

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QY      1 ACRTGNGAYTCNGTRTA 17
          ||:||:||:||:||
Db     314 ACGTCGGAATTCGTATA 330
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**RESULT**    **4**

LOCUS					
BJ052660	416 bp	mRNA	linear	EST	11-DEC-20
BJ052660	NIBB Mochii normalized xenopus neurula library	xenopus			
DEFINITION					
Xenopus laevis cDNA clone Xl042d117, 416 nucleotides.					

ACCESSION	BJ052600
VERSION	BJ052660.1
KEYWORDS	GI:17498706
	EST.

ORGANISM  
Xenopus laevis  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Xenopodinae; Xenopus.  
1 (bases 1 to 416)

TITLE  
JOURNAL,  
Expressed genes in *X. laevis* embryo  
Unpublished (2001)  
, Y.

CONTACT: JACQUES SHIM-1  
Center For Genetic Resource Information  
National Institute of Genetics

Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: [tshini@genes.nig.ac.jp](mailto:tshini@genes.nig.ac.jp).

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 02:15:49 ; Search time 2591.91 Seconds  
(without alignments)  
88.525 Million cell updates/sec

Title: us-09-724-841-10  
Sequence: 1 ACRTGNGATTCNGTCTTA 17

Scoring table: IDENTITY-NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estinu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_nlc:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.8	81.2	301	9	AW788294 C00336-F
2	13.8	81.2	352	9	AV705097 AV705097
3	13.8	81.2	405	10	BF887255 CM4-TN014
4	13.8	81.2	416	10	BJ052660 BJ052660
5	13.8	81.2	419	12	B53166 CIT-HSP-200
6	13.8	81.2	470	10	BC017447 de64b12.x
7	13.8	81.2	472	10	BM191868 dag37f01.
8	13.8	81.2	478	9	AI380969 tg18d12.x
9	13.8	81.2	502	10	BE543117 601069058
10	13.8	81.2	518	12	AL177124 Fugu rubr
11	13.8	81.2	528	9	AW766896 da61d11.y
12	13.8	81.2	556	9	AA034789 m153d05.x
13	13.8	81.2	573	10	BI341029 368222 MA
14	13.8	81.2	583	12	AL127134 Fugu rubr
15	13.8	81.2	597	12	FR0039639 Fugu rubr
16	13.8	81.2	599	12	AL127150 Fugu rubr
17	13.8	81.2	609	12	FR0039649 AL127144 Fugu rubr

C 18	13.8	81.2	643	10	W98391	W98391 m020a05.r1
C 19	13.8	81.2	726	10	BC306142	BC306142 fm52g08.x
C 20	13.8	81.2	738	12	A2184518	A2184518 SP-1003-A
C 21	13.8	81.2	750	12	BH327893	BH327893 CH230-124
C 22	13.8	81.2	789	10	BG823603	BG823603 602728993
C 23	13.8	81.2	848	9	AI322582	AI322582 m153d05.y
C 24	13.8	81.2	863	9	AU119404	AU119404 AU119404
C 25	13.8	81.2	962	12	CNS01XNS	AL171937 Tetradon
C 26	13.8	81.2	1036	12	CNS050RX	AL49668 Tetradon
C 27	13.8	81.2	1547	12	AG031697	AG031697 Pan. Etrog1
C 28	12.8	75.3	153	10	BG609709	BG609709 323656 MA
C 29	12.8	75.3	212	9	BB348982	BB348982 BB348982
C 30	12.8	75.3	215	10	BG450224	BG450224 NF015E10D
C 31	12.8	75.3	219	9	AA035435	AA035435 zk25f11.r
C 32	12.8	75.3	220	10	BE350988	BE350988 ht22b05.x
C 33	12.8	75.3	234	9	AA716548	AA716548 z970c04.s
C 34	12.8	75.3	234	10	BE827388	BE827388 CM2-ET001
C 35	12.8	75.3	235	12	BH354835	BH354835 CH230-331
C 36	12.8	75.3	247	9	AW312889	AW312889 5259 MARC
C 37	12.8	75.3	253	12	BH185768	BH185768 028.M.03-
C 38	12.8	75.3	253	12	CNS070EJ	AL622217 T3 end of
C 39	12.8	75.3	259	10	Z21283	Z21283 HSNADMXU T
C 40	12.8	75.3	260	9	AV266760	AV266760 AV266760
C 41	12.8	75.3	262	10	BM071779	BM071779 fu87g11.x
C 42	12.8	75.3	263	10	BE846090	BE846090 232309 BA
C 43	12.8	75.3	264	9	BI119275	BI119275 BI119275
C 44	12.8	75.3	265	10	BI38396	BI38396 1c22608.Y
C 45	12.8	75.3	276	9	AV143032	AV143032 AV143032

## ALIGNMENTS

RESULT 1	AW788294	301 bp	mrna	linear	EST 01-MAY-2001
LOCUS	C00336-F	Lambda Zap, StrataGene	Blumeria graminis f. sp. hordei		
DEFINITION	CDNA clone C00336, mRNA sequence.				
ACCESSION	AW788294.1	GI:13899891			
VERSION	AW788294				
KEYWORDS	EST.				
SOURCE	Blumeria graminis f. sp. hordei.				
ORGANISM	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Erysiphales; Erysiphaceae; Blumeria.				
REFERENCE	1 (bases 1 to 301)				
AUTHORS	Thomas,S.W., Rasmussen,S.W., Glaring,M.A., Rouster,J.A. and Oliver				
TITLE	R.P. Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Rasmussen,S.W. Department of Yeast Genetics Carlsberg Laboratory 10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark Tel: 45 3327 5230 Fax: 45 3327 4766 Email: svr@erc.dk High quality sequence stop: 301 POLYA-NO.				
FEATURES	Location/Qualifiers				
source	1..301				
	/organism="Blumeria graminis f. sp. hordei"				
	/db_xref="taxon:62688"				
	/clone_id="C00336"				
	/clone_lib="Lambda Zap, StrataGene"				
	/cell_type="conidia"				
	/lab_host="Hordeum vulgare"				
BASE COUNT	94 a 72 c 59 g 75 t				
ORIGIN	1 others				
Query Match	81.2%; Score 13.8; DB 9; Length 301;				







DE Streptococcus pneumoniae pbp1A TER isolate g) nucleotide sequence.  
 XX  
 KW Streptococcus pneumoniae; penicillin binding protein: pbp2B; pbp1A;  
 KM transpeptidase encoding region; TER; antibiotic resistance; diagnosis;  
 XX detection; identification; pneumococcal meningitis; ss.  
 OS Streptococcus pneumoniae.  
 XX  
 PN ZA9807024-A.  
 PD 28-APR-1999.  
 XX  
 PF 05-AUG-1998: 982A-0007024.  
 PR 01-AUG-1997: 972A-0006886.  
 XX  
 PA (SAME-) SOUTH AFRICAN INST MEDICAL RES.  
 PA (UYWI-) UNIV WITWATERSRAND.  
 PA (MEDI-) MEDICAL RES COUNCIL.  
 XX  
 PI Klugman KP, Smith AM, Du Plessis M;  
 DR WPI: 1999-601770/51.  
 XX  
 PT Polymerase chain reaction assays for detecting Streptococcus pneumonia  
 useful for the diagnosis of pneumococcal meningitis -  
 XX  
 PS Claim 11: Fig 4: 63pp: English.  
 XX  
 CC A polymerase chain reaction (PCR) assays have been developed for  
 detecting an antibiotic resistant strain of Streptococcus pneumoniae  
 using primers based on the penicillin binding protein 2B (pbp2B) gene  
 and the pbp1A gene. The products and methods can be used for detecting  
 S. pneumoniae, particularly antibiotic-resistant strains. They can be  
 used for simultaneously diagnosing pneumococcal meningitis and  
 identifying any antibiotic-resistant S. pneumoniae strains in a sample.  
 The methods can be used for detecting S. pneumoniae strains resistant  
 to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin.  
 The assays can be adapted to detect other pathogens causing meningitis.  
 S. pneumoniae with a minimum inhibitory concentration (MIC) of  
 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and  
 a 224 bp product. The present sequence represents a Streptococcus  
 pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide  
 sequence from the present invention.  
 CC  
 XX  
 SQ Sequence 1260 BP; 404 A; 281 C; 268 G; 307 T; 0 other;  
 Query Match 81.2%; Score 13.8; DB 20; Length 1260;  
 Best Local Similarity 70.6%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 ACRTGCGAYTCNGTRTA 17  
 Db 903 ACGTCGATTCGCTATA 887  
 AAZ35946/C  
 ID AAZ35946 standard; DNA: 1260 BP.  
 XX  
 AC AAZ35946;  
 XX  
 DT 07-FEB-2000 (first entry)  
 XX  
 DE Streptococcus pneumoniae pbp1A TER isolate h) nucleotide sequence.  
 XX  
 KW Streptococcus pneumoniae; penicillin binding protein: pbp2B; pbp1A;  
 KM transpeptidase encoding region; TER; antibiotic resistance; diagnosis;  
 XX detection; identification; pneumococcal meningitis; ss.  
 OS Streptococcus pneumoniae.

XX  
 PN ZA9807024-A.  
 XX  
 PD 28-APR-1999.  
 XX  
 PF 05-AUG-1998: 982A-0007024.  
 PR 01-AUG-1997: 972A-0006886.  
 XX  
 PA (SAME-) SOUTH AFRICAN INST MEDICAL RES.  
 PA (UYWI-) UNIV WITWATERSRAND.  
 PA (MEDI-) MEDICAL RES COUNCIL.  
 XX  
 PI Klugman KP, Smith AM, Du Plessis M;  
 DR WPI: 1999-601770/51.  
 XX  
 PT Polymerase chain reaction assays for detecting Streptococcus pneumonia  
 useful for the diagnosis of pneumococcal meningitis -  
 XX  
 PS Claim 11: Fig 4: 63pp: English.  
 XX  
 CC A polymerase chain reaction (PCR) assays have been developed for  
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 The methods can be used for detecting S. pneumoniae strains resistant  
 to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin.  
 The assays can be adapted to detect other pathogens causing meningitis.  
 S. pneumoniae with a minimum inhibitory concentration (MIC) of  
 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and  
 a 224 bp product. The present sequence represents a Streptococcus  
 pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide  
 sequence from the present invention.  
 CC  
 XX  
 SQ Sequence 1260 BP; 406 A; 284 C; 267 G; 303 T; 0 other;  
 Query Match 81.2%; Score 13.8; DB 20; Length 1260;  
 Best Local Similarity 70.6%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 ACRTGCGAYTCNGTRTA 17  
 Db 903 ACGTCGATTCGCTATA 887  
 AAZ35946/C  
 ID AAZ35946 standard; DNA: 1260 BP.  
 XX  
 AC AAZ35946;  
 XX  
 DT 07-FEB-2000 (first entry)  
 XX  
 DE Streptococcus pneumoniae pbp1A TER isolate h) nucleotide sequence.  
 XX  
 KW Streptococcus pneumoniae; penicillin binding protein: pbp2B; pbp1A;  
 KM transpeptidase encoding region; TER; antibiotic resistance; diagnosis;  
 XX detection; identification; pneumococcal meningitis; ss.  
 OS Streptococcus pneumoniae.

Search completed: June 19, 2002, 02:20:52  
 Job time: 5410 sec

OY 1 ACRTGCAATTCNGTCTA 17  
DB 717 ACGTCGATTCGCTATA 701

RESULT 12  
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AC AAZ35943;  
XX  
XX  
XX 07-FEB-2000 (first entry)

DE Streptococcus pneumoniae pbp1A TER isolate e) nucleotide sequence.  
XX  
XX Streptococcus pneumoniae; penicillin binding protein; pbp2B; pbp1A;  
KM transpeptidase encoding region; TER; antibiotic resistance; diagnosis;  
XX detection; identification; pneumococcal meningitis; ss.

OS Streptococcus pneumoniae.

PN ZAG807024-A.

XX 28-APR-1999.

PD 05-AUG-1998; 982A-0007024.

PF 01-AUG-1997; 972A-0006886.

PR (SAME-) SOUTH AFRICAN INST MEDICAL RES.  
(UYWI-) UNIV WITWATERSRAND.

PA (MEDI-) MEDICAL RES COUNCIL.

PI Klugman KP, Smith AM, Du Plessis M;

XX WPI: 1999-601770/51.

DR Polymerase chain reaction assays for detecting Streptococcus pneumonia  
XX useful for the diagnosis of pneumococcal meningitis

PS Claim 11; Fig 4; 63pp; English.

CC A polymerase chain reaction (PCR) assays have been developed for  
CC detecting an antibiotic resistant strain of Streptococcus pneumoniae  
CC using primers based on the penicillin binding protein 2B (pbp2B) gene  
CC and the pbp1A gene. The products and methods can be used for detecting  
CC S. pneumoniae, particularly antibiotic-resistant strains. They can be  
CC used for simultaneously diagnosing pneumococcal meningitis and  
CC identifying any antibiotic-resistant S. pneumoniae strains in a sample.  
CC The methods can be used for detecting S. pneumoniae strains resistant  
CC to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin.  
CC The assays can be adapted to detect other pathogens causing meningitis.  
CC The assays can be used to detect an antibiotic resistant strain of  
CC S. pneumoniae with a minimum inhibitory concentration (MIC) of  
CC 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and  
CC a 224 bp product. The present sequence represents a Streptococcus  
CC pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide  
CC sequence from the present invention.

XX Sequence 1260 BP; 408 A; 286 C; 263 G; 303 T; 0 other;

Query Match 81.2%; Score 13.8; DB 20; Length 1260;  
Best Local Similarity 70.6%; Pred. No. 1.3e+02;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGCAATTCNGTCTA 17  
DB 903 ACGTCGATTCGCTATA 887

RESULT 13

AAZ35944/C  
ID AAZ35944 standard; DNA: 1260 BP.

AC AAZ35944;

XX 07-FEB-2000 (first entry)

DE Streptococcus pneumoniae pbp1A TER isolate f) nucleotide sequence.

XX Streptococcus pneumoniae; penicillin binding protein; pbp2B; pbp1A;  
KM transpeptidase encoding region; TER; antibiotic resistance; diagnosis;  
XX detection; identification; pneumococcal meningitis; ss.

OS Streptococcus pneumoniae.

PN ZAG807024-A.

XX 28-APR-1999.

PD 05-AUG-1998; 982A-0007024.

PF 01-AUG-1997; 972A-0006886.

PR (SAME-) SOUTH AFRICAN INST MEDICAL RES.  
(UYWI-) UNIV WITWATERSRAND.

PA (MEDI-) MEDICAL RES COUNCIL.

PI Klugman KP, Smith AM, Du Plessis M;

XX WPI: 1999-601770/51.

DR Polymerase chain reaction assays for detecting Streptococcus pneumonia  
XX useful for the diagnosis of pneumococcal meningitis

PS Claim 11; Fig 4; 63pp; English.

CC A polymerase chain reaction (PCR) assays have been developed for  
CC detecting an antibiotic resistant strain of Streptococcus pneumoniae  
CC using primers based on the penicillin binding protein 2B (pbp2B) gene  
CC and the pbp1A gene. The products and methods can be used for detecting  
CC S. pneumoniae, particularly antibiotic-resistant strains. They can be  
CC used for simultaneously diagnosing pneumococcal meningitis and  
CC identifying any antibiotic-resistant S. pneumoniae strains in a sample.  
CC The methods can be used for detecting S. pneumoniae strains resistant  
CC to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin.  
CC The assays can be adapted to detect other pathogens causing meningitis.  
CC The assays can be used to detect an antibiotic resistant strain of  
CC S. pneumoniae with a minimum inhibitory concentration (MIC) of  
CC 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and  
CC a 224 bp product. The present sequence represents a Streptococcus  
CC pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide  
CC sequence from the present invention.

XX Sequence 1260 BP; 403 A; 291 C; 267 G; 299 T; 0 other;

Query Match 81.2%; Score 13.8; DB 20; Length 1260;  
Best Local Similarity 70.6%; Pred. No. 1.3e+02;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGCAATTCNGTCTA 17  
DB 903 ACGTCGATTCGCTATA 887

RESULT 14  
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AC AAZ35945;

XX 07-FEB-2000 (first entry)

XX

XX AAC98828;  
 AC AH01023/c  
 DT AH01023 standard; DNA; 1199 BP.  
 XX  
 DE 09-MAR-2001 (first entry)  
 XX  
 DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:56.  
 KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen;  
 KW detection; diagnosis; identification; cytotoxic; neuroprotective;  
 KW neoplastic; immunomodulatory; relaxant; contraceptive; gynaecological;  
 KW antiinflammatory; cardiac; gene therapy; chromosome mapping;  
 KW linkage analysis; tissue identification; tissue typing; forensic;  
 KW neural; immune system; muscular; reproductive; gastrointestinal;  
 KW pulmonary; cardiovascular; renal; proliferative; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN M020055320-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PE 08-MAR-2000; 2000WO-US05989.  
 XX  
 PR 12-MAR-1999; 99US-0124270.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI: 2000-579444/54.  
 DR P-PSDB: AAB54063.  
 XX  
 PT New nucleic acid that is a pancreatic cancer antigen for preventing,  
 PT treating, or ameliorating a medical condition, particular pancreatic  
 PT cancer, or for use in assays for diagnosing a pathological condition -  
 XX  
 XX Claim 1; Page 535; 1379pp; English.  
 XX  
 CC AAC98773 to AAC99231 encode the human pancreatic cancer associated  
 CC proteins, called pancreatic cancer antigens, given in AAB54408 to  
 CC AAB54466. The human pancreatic cancer antigens have cytostatic,  
 CC neuroprotective, neoplastic, immunomodulatory, relaxant, contraceptive,  
 CC gynaecological, cardiac and antiinflammatory activities, and can be used  
 CC in gene therapy. The polynucleotide and proteins can be used for  
 CC preventing, treating, or ameliorating a medical condition or in assays  
 CC for diagnosing a pathological condition or a susceptibility to one in a  
 CC subject. Binding partners to the proteins and the activity of the  
 CC proteins can be identified. The pancreatic cancer antigens can be used to  
 CC detect, treat or prevent pancreatic disorders, especially cancer.  
 CC Agonists and antagonists to the antigens can be screened for. The  
 CC pancreatic cancer antigen polynucleotides can be used to design nucleic  
 CC acid hybridisation probes that can be used in chromosome mapping, linkage  
 CC analysis, tissue identification and/or typing in a variety of forensic  
 CC and diagnostic methods. The proteins can be used to generate antibodies  
 CC which are used to purify, detect and target the polypeptides, including  
 CC both in vivo and in vitro diagnostic and therapeutic methods. The  
 CC proteins can be used to treat or prevent neural, immune system, muscular,  
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or  
 CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent  
 CC sequences used in the exemplification of the present invention.  
 CC  
 XX Sequence 1140 BP; 297 A; 271 C; 293 G; 275 T; 4 other;  
 SO

Query Match 81.2%; Score 13.8; DB 21; Length 1140;  
 Best Local Similarity 70.6%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

1 ACRICNGAYTNGRTTA 17  
 11:11 11:11 11:11  
 534 ACGTCGATCTGTATA 518

RESULT 11  
 ID AH01023/c  
 XX AH01023 standard; DNA; 1199 BP.  
 AC AH01023;  
 XX  
 DE 24-JUL-2001 (first entry)  
 XX  
 DE Streptococcus pneumoniae nucleotide sequence SEQ ID NO:1014.  
 KW Streptococcus pneumoniae; Streptococcus pneumoniae;  
 KW identification; algal; archaeal; bacterial; fungal; parasitical;  
 KW microorganism; diagnosis; translation elongation factor Tu; toxin;  
 KW translation elongation factor G; RecA recombinase; resistance;  
 KW catalytic subunit of proton-translocating ATPase; antimicrobial;  
 KW vaccine; primer; ds.  
 XX  
 OS Streptococcus pneumoniae.  
 XX  
 PN M0200123604-A2.  
 XX  
 PD 05-APR-2001.  
 XX  
 PE 28-SEP-2000; 2000WO-CA01150.  
 XX  
 PR 28-SEP-1999; 99CA-2283458.  
 XX  
 PR 19-MAR-2000; 2000CA-2307010.  
 XX  
 PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.  
 XX  
 PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M,  
 PI Picard FJ, Roy PH;  
 XX  
 DR WPI: 2001-245006/25.  
 XX  
 PT Nucleic acid sequences are used to generate universal probes and  
 PT primers which can be used to identify and detect the presence of algal,  
 PT archaeal, bacterial, fungal and parasitical species in a test sample -  
 XX  
 XX Claim 27; Page 968; 1580pp; English.  
 XX  
 CC The present invention describes a method for generating a repository of  
 CC nucleic acids of tuf, fus, atp and/or recA genes from which probes  
 CC and/or primers are derived. The method comprises amplifying the nucleic  
 CC acids of determined algal, archaeal, bacterial, fungal and parasitical  
 CC species with a combination of defined primer pairs. The method can be  
 CC used for producing probes and/or primers for detecting one or more  
 CC related microorganisms e.g. algae, archaea, bacteria, fungi and  
 CC parasites, for universal detection and for specific and ubiquitous  
 CC detection and identification of an algal, archaeal, bacterial, fungal  
 CC and parasitical species, genus, family and group. A nucleic acid (I)  
 CC obtained using the method of the invention can be used for the universal  
 CC detection of any bacterium, fungus or parasite in a sample and for the  
 CC detection of at least one antimicrobial agent resistance gene or at  
 CC least one toxin gene. hexa nucleic acids are used for the specific and  
 CC ubiquitous detection and for identification of Streptococcus pneumoniae.  
 CC (I) can be used to design a therapeutic agent which is effective against  
 CC microorganisms. Microbial species or genus or family or phylum or group  
 CC which can be detected include Abiotrophia adiacens, Bordetella sp.,  
 CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,  
 CC Mycobacteriaceae family, Pseudomonas group, Streptococcus sp.,  
 CC Neisseria gonorrhoeae and Staphylococcus sp. Using DNA based tests  
 CC provides faster results than substrate specificity tests as results can  
 CC be determined in an hour and improved accuracy is also achieved.  
 CC AH000010 to AH0002304 represent nucleotide sequences and primers/probes  
 CC which are given in the exemplification of the present invention.  
 CC  
 XX Sequence 1199 BP; 386 A; 286 C; 240 G; 287 T; 0 other;  
 SO

Query Match 81.2%; Score 13.8; DB 22; Length 1199;  
 Best Local Similarity 70.6%; Pred. No. 1.3e+02;  
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

## RESULT 8

AAFS7022  
ID AAF57022 standard; DNA; 17 BP.

XX AAF57022;

DT 14-MAY-2001 (first entry)

DE Simian ETF cDNA specific degenerate primer.

XX Epithelium-derived T-cell factor; ETF; simian; human; enteritis;

KW gastrointestinal disease; mucositis; peptic ulcer; cytostatic;

KW villus atrophic disorder; inflammatory bowel disease; antiinflammatory;

KW anti-HIV; antiviral; T-lymphocyte stimulator; PCR primer; ss.

OS Synthetic.

PN US6184359-B1.

PD 06-FEB-2001.

PF 09-NOV-1998; 98US-0189193.

XX 22-FEB-1995; 95US-0393305.

PR 04-OCT-1996; 96US-0725969.

PR 08-MAR-1993; 93US-0031399.

PR 22-APR-1994; 94US-0233606.

PA (IMV) IMMUNEX CORP.

PI Grabstein KH, Anderson DM, Eisenman JR, Fung V, Rauch C;

XX WPI; 2001-217801/22.

XX New antibodies that specifically binds epithelium-derived T-cell factor

PT polypeptide useful for e.g. treating or preventing gastrointestinal

PT diseases, HIV and HIV-associated diseases, augmenting destruction of

PT tumour cells

XX Example 3; Column 25; 35pp; English.

XX The invention relates to simian and human epithelium-derived T-cell

CC factor (ETF) polypeptides. Antibodies that specifically bind to the ETF

CC polypeptides are used for treating or preventing gastrointestinal

CC diseases, such as chemotherapy and radiation therapy-induced enteritis

CC and mucositis, peptic ulcer disease, villus atrophic disorders and

CC inflammatory bowel disease; for increasing tolerated doses for radiation

CC therapy and chemotherapy agents which are limited by gastrointestinal

CC toxicity; and for treating HIV and HIV-associated diseases. The

CC antibodies are further used to treat a variety of other diseases or

CC conditions where it is desired to stimulate proliferation of

CC T-lymphocytes and B lymphocytes, or the secretion of immunoglobulin B

CC lymphocytes, to augment anti-infectious disease immunity, to induce CTL,

CC LAK or NK lytic activity, or to augment the destruction of tumour cells

CC or cells infected with virus. Sequences AAF57021-23 represent PCR primers

CC used for simian ETF (ETF) cDNA cloning.

XX Sequence 17 BP; 3 A; 3 C; 2 G; 4 T; 5 other;

SO

Query Match 81.2%; Score 13.8; DB 22; Length 17;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGCAATCNGTCTTA 17

DB 1 acrtgcaatcngtcttta 17

RESULT 9  
AAS65068/c

ID AAS65068 standard; CDNA; 631 BP.

XX AAS65068;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #872.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PADB; ABG00881.

XX Claim 1; SEQ ID No 872; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful for treating

CC disorders involving aberrant protein expression or biological activity.

CC the polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human

CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 631 BP; 99 A; 196 C; 158 G; 178 T; 0 other;

SO

Query Match 81.2%; Score 13.8; DB 23; Length 631;

Best Local Similarity 70.6%; Pred. No. 1.2e+02;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGCAATCNGTCTTA 17

DB 234 ACRTGCAATCNGTCTTA 218

RESULT 10  
AAC98828/c  
ID AAC98828 standard; CDNA; 1140 BP.

AAZ38247;  
 ID AAZ29484 standard; DNA; 17 BP.  
 AC AAZ29484;  
 XX  
 XX  
 DT 10-JUN-1999 (first entry)  
 DE Simian ETF DNA amplifying primer.  
 XX  
 XX  
 DE Epithelium-derived T-cell factor; ETF; immunoassay; enteritis; ulcer;  
 KW T cell proliferation; gastrointestinal disease; mucositis; colitis;  
 KW gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease;  
 KW human immune deficiency virus; tumour; simian; PCR primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US5892001-A.  
 XX  
 PD 06-APR-1999.  
 XX  
 PF 04-OCT-1996; 96US-0725969.  
 XX  
 PR 22-FEB-1995; 95US-0393305.  
 PR 08-MAR-1993; 93US-0031399.  
 PR 22-APR-1994; 94US-0233606.  
 PR 04-OCT-1996; 96US-0725969.  
 XX  
 XX (IMNV ) IMMUNEX CORP.  
 PA  
 PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
 PI Rauch C;  
 XX  
 DR WPI: 1999-253930/21.  
 XX  
 PT Antibodies specific for epithelium-derived T-cell growth factor  
 PS  
 XX Example 3; Columns 25; 34pp; English.  
 CC The invention relates to an isolated antibody that binds specifically to  
 CC a simian or human epithelium-derived T-cell factor (ETF) polypeptide.  
 CC The antibodies are used, optionally when immobilized or labeled, to  
 CC detect and quantify ETF in standard immunoassays. They may also be used  
 CC as diagnostic and therapeutic agents, e.g. when conjugated to toxins (or  
 CC their precursors) or radionuclides. ETF induces proliferation and/or  
 CC differentiation of T cells (or their precursors), e.g. for use in  
 CC establishing long term in vitro cultures; and is also used to treat  
 CC gastrointestinal disease (e.g. enteritis or mucositis induced by  
 CC chemotherapy or radiation, peptide ulcer, gastroenteritis, colitis,  
 CC villus atrophy, malignancy and inflammatory bowel disease), to treat  
 CC human immune deficiency virus infection or associated disease, or  
 CC generally in any situation requiring stimulation of T or B cell  
 CC proliferation, secretion of immunoglobulins or certain cytokines,  
 CC increased anti-infectious disease immunity, induction of T-cell lytic  
 CC activity or increased destruction of tumour or virus-infected cells.  
 CC Sequences AAZ29483-85 represent primers for PCR amplification of the  
 CC simian ETF DNA sequences.  
 CC  
 CC Sequence 17 BP; 3 A; 3 C; 2 G; 4 T; 5 other;  
 SO  
 Query Match 81.2%; Score 13.8; DB 20; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 83;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 ACRTGCAATGCTGRTA 17  
 DB 1 acrtngaytcngtrta 17  
 ||||||||||||||||  
 RESULT 7  
 ID AAZ38247  
 ID AAZ38247 standard; DNA; 17 BP.  
 XX

AAZ38247;  
 AC AAZ38247;  
 XX  
 DT 09-FEB-2000 (first entry)  
 DE Simian ETF degenerate PCR primer #10.  
 XX  
 XX  
 DE ETF; epithelium-derived T-cell factor; T-cell; T-lymphocyte;  
 KW proliferation; differentiation; growth factor; precursor; mature; CD4+;  
 KW CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;  
 KW gastrointestinal disease; gastroenteritis; colitis;  
 KW inflammatory bowel disease; villus atrophic disorder; enteritis;  
 KW chemotherapy; radiotherapy; gut toxicity; cancer; side effect;  
 KW tolerated dose; PCR; primer; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN Mammalia.  
 XX  
 PD US5985262-A.  
 XX  
 PF 16-NOV-1999.  
 XX  
 PR 03-FEB-1997; 97US-0794524.  
 XX  
 PR 22-FEB-1995; 95US-0393305.  
 PR 04-OCT-1996; 96US-0726817.  
 PR 08-MAR-1993; 93US-0031399.  
 PR 22-APR-1994; 94US-0233606.  
 XX  
 XX (IMNV ) IMMUNEX CORP.  
 PA  
 PI Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;  
 PI  
 XX  
 DR WPI: 2000-022267/02.  
 DR P-PSDB: AAZ52313.  
 XX  
 PT Stimulation of T-cells in human immunodeficiency virus infected  
 PT patients -  
 PS  
 XX Example 3; Column 25; 33pp; English.  
 CC This sequence represents simian ETF degenerate PCR primer #10,  
 CC used with degenerate primer #9 (AAZ38246) to amplify a fragment  
 CC of the gene encoding simian epithelium-derived T-cell factor (ETF).  
 CC This was used to probe a simian cDNA library for a clone with a  
 CC complete open reading frame (AAZ38224). The primers were based on  
 CC N-terminal amino acid sequences in the purified ETF protein.  
 CC ETF is a previously unidentified T-cell growth factor which  
 CC stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to  
 CC proliferate and differentiate. It also promotes proliferation of the  
 CC gastrointestinal epithelium. The protein can be used to promote long-term  
 CC in vitro culture of T-lymphocytes and T-cell lines. ETF can be used for  
 CC treating HIV infection, HIV-associated diseases, and other diseases or  
 CC conditions where stimulation of T-cell proliferation would be desirable  
 CC e.g., it could be used to augment the destruction of tumour cells or  
 CC vitally- infected cells. ETF may also be used to treat or prevent  
 CC gastrointestinal disease, including chemotherapy and radiotherapy  
 CC associated enteritis, gastroenteritis, colitis, inflammatory bowel  
 CC disease and villus atrophic disorders. Chemotherapy and radiotherapy  
 CC associated enteritis (gut toxicity) results in bleeding and sepsis due to  
 CC gastrointestinal flora entering the blood, and thus can limit the dosage  
 CC of therapeutic agent administered to a cancer patient. ETF may therefore  
 CC be used to increase the tolerated doses radiotherapy and chemotherapy.  
 CC  
 CC Sequence 17 BP; 3 A; 3 C; 2 G; 4 T; 5 other;  
 SO  
 Query Match 81.2%; Score 13.8; DB 21; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 83;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 ACRTGCAATGCTGRTA 17  
 DB 1 acrtngaytcngtrta 17  
 ||||||||||||||||

CC CVI/EBNA cDNA library for the full-length SEF coding sequence.  
 CC Mature SEF induces proliferation and/or differentiation of precursor  
 CC or mature T cells and is useful for promoting long-term in vitro  
 CC culture of T-lymphocytes and T-cell lines. It is used for treating  
 CC gastrointestinal diseases including peptic ulcer, colitis and  
 CC malignancy and for treating HIV infection.

XX Sequence 17 BP; 3 A; 3 C; 2 G; 4 T; 5 other;

Query Match 81.2%; Score 13.8; DB 17; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 83;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGCAATCNGTCTTA 17  
 ||||||||||||||||  
 DB 1 acrtgngaytcngtrta 17

## RESULT 4

AAAT42245  
 ID AAT42245 standard; DNA; 17 BP.

AC AAT42245;

DT 05-FEB-1997 (first entry)

DE Simian ETF gene primer #1 based on amino acids 26-31 of mature ETF.

XX Epithelium-derived T-cell factor; simian; human; culture; proliferation;  
 KW epithelial cell; differentiation; T-lymphocyte; African green monkey;

KW primer; PCR; polymerase chain reaction; amplification; probe; ss.

XX Synthetic.

XX US5552303-A.

PD 03-SEP-1996.

PF 08-MAR-1993; 93US-0031399.

PR 08-MAR-1993; 93US-0031399.

PA (IMMV) IMMUNEX CORP.

PI Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;

DR WPI; 1996-412063/41.

PT New isolated simian and human epithelium-derived T-cell factors -  
 PT which stimulate the proliferation and/or differentiation of  
 PT T-lymphocytes and T-cell lines

XX Example 3; Column 17; 22pp; English.

XX Primers AAT42244-6 were used to amplify a 92 bp fragment of the African  
 CC green monkey epithelium-derived T-cell factor (ETF; AAT42243). The  
 CC sequence of this primer is based on amino acids 26-31 of the mature ETF  
 CC protein sequence obtained by peptide sequencing the purified protein.  
 CC The template for the amplification was cDNA derived from monkey kidney  
 CC CV-1/EBNA cells stimulated to proliferate by phorbol 12-myristate  
 CC 13-acetate. The 92 bp fragment was labelled and used as a probe to  
 CC isolate a clone C85.SEF which contained the simian gene. ETF is a  
 CC protein of 15-17 kD which is expressed by epithelial cells and  
 CC stimulates proliferation and/or differentiation of precursor and/or  
 CC mature T cells. The protein is therefore useful for promoting long term  
 CC in vivo culture of T-lymphocytes and T-cell lines.

XX Sequence 17 BP; 3 A; 3 C; 2 G; 4 T; 5 other;

Query Match 81.2%; Score 13.8; DB 17; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 83;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGCAATCNGTCTTA 17  
 ||||||||||||||||  
 DB 1 acrtgngaytcngtrta 17

## RESULT 5

AAV02876  
 ID AAV02876 standard; DNA; 17 BP.

AC AAV02876;

DT 08-MAY-1998 (first entry)

DE Simian epithelium derived T-cell factor PCR primer 2.

XX Epithelium derived T-cell factor; ETF; simian; gastrointestinal disease;  
 KW B-cell stimulation; epithelium; villi; CD4+; CD8+; T-cell stimulation;  
 KW treatment; prevention; PCR primer; ss.

XX Synthetic.

XX Simian.

XX US5707616-A.

PD 13-JAN-1998.

PF 04-OCT-1996; 96US-0726817.

PR 22-FEB-1995; 95US-0393305.

PR 08-MAR-1993; 93US-0031399.

PR 22-APR-1994; 94US-0233606.

PA (IMMV) IMMUNEX CORP.

PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;

PT Rauch C;

PT Treatment or prevention of gastrointestinal diseases - by  
 PT administering epithelium-derived T-cell factor polypeptide

XX Example 3; Column 41-42; 34pp; English.

XX PCR primers AAV02875-V02877 are used in the amplification of a simian  
 CC epithelium-derived T-cell factor (ETF) which is used in a method for  
 CC treating or preventing gastrointestinal disease. These polypeptides have  
 CC particular application in the treatment of gastrointestinal disorders  
 CC associated with disruption of the gastrointestinal epithelium or villi  
 CC such as chemotherapy- and radiation-therapy induced enteritis (gut  
 CC toxicity), mucositis, peptic ulcer disease, gastroenteritis and colitis,  
 CC villus atrophic disorders, malignancy and inflammatory bowel disease.  
 CC ETF polypeptides may also be useful in the treatment of human  
 CC immunodeficiency virus (HIV) and HIV-associated disease due to their  
 CC ability to stimulate CD4+ and CD8+ cells. Biologically active ETF may be  
 CC used to treat a variety of other diseases or conditions where T-cell or  
 CC B-cell stimulation is desired.

XX Sequence 17 BP; 3 A; 3 C; 2 G; 4 T; 5 other;

Query Match 81.2%; Score 13.8; DB 19; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 83;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGCAATCNGTCTTA 17  
 ||||||||||||||||  
 DB 1 acrtgngaytcngtrta 17

## RESULT 6



XX WPI: 1995-373556/48.

DR Isolated DNA encoding polypeptide with mammalian IL-15 activity - which  
XX stimulates proliferation and differentiation of T cells, used for  
PT treating carcinoma(s), melanomas, etc. and viral infections  
PS

XX Example: Page 21; 48pp; English.

CC A simian species of IL-15 (sIL-15) was purified and analysed by SDS-  
CC PAGE. Bioassay of unstained gel slices indicated IL-15 activity was  
CC assoc. with proteins having mol. wts in the range of 15-17 kDa. The  
CC N-terminus of the first 33 AAs of AAR83309. The results indicated the  
CC identity of the first 33 AAs of AAR83309. Subsequent sequencing of a  
CC cDNA clone obt. from a simian library provided a sequence encoding  
CC the polypeptide AAR83436. AAR83436 comprises a relatively short 48 AA  
CC leader sequence and a mature polypeptide AAR83309. The sequence of the  
CC N-terminal 31 AAs of AAR83309 was used to design synthetic PCR primers  
CC for the amplification of IL-15-specific DNA sequences. The first  
CC 6 AAs of the N-terminus were used to design one primer, a  
CC degenerate mixture coding for all possible codon usages - AAT00528.  
CC The AA sequences of the simian mature N-terminus 26-31 were used  
CC to design a second primer, a degenerate mixture coding for a  
CC complement of all possible codon usages of AAs 26-31, omitting  
CC posn. 3 of Val (AAT00529, AAT00530). Polyadenylated RNAs from CV-1/EBNA  
CC cells were used as templates. A 92 bp DNA fragment was used as a  
CC hybridism. probe to screen a portion of a plasmid library contg.  
CC cDNA inserts prepd. from CV-1/EBNA polyadenylated RNA. This  
CC resulted in the isolation of clone C85, sIL-15 that has an ORF  
CC given in AAT00524. AAR83309 is the active polypeptide & AAR83436 is  
CC the precursor polypeptide.

XX Sequence 17 BP; 3 A; 3 C; 2 G; 4 T; 5 other;

SO Query Match 81.2%; Score 13.8; DB 16; Length 17;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTCNGAYTCNGTCTTA 17  
|||||  
Db 1 acrtcngaytcngtctta 17

RESULT 2

AA084586 ID AA084586 standard; cDNA; 17 BP.

XX AA084586;

AC 04-SEP-1995 (first entry)

XX Simian IL-15 primer.

DE Interleukin-15; IL-15; sIL-15; T-cell growth factor;  
KM African green monkey; CV-1; antitumor; virucide; primer; PCR;  
KW polymerase chain reaction; ss.

XX Synthetic.

OS ZA9402636-A.

XX ZA9402636-A.

XX 28-DEC-1994.

XX 18-APR-1994; 94ZA-0002636.

XX 18-APR-1994; 94ZA-0002636.

XX (IMMV) IMMUNEX CORP.

PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
PI Rauch C;  
XX

DR WPI: 1995-082473/11.

XX New purified interleukin-15 - which induces T cell proliferation  
PT and differentiation, used for the treatment of tumours and viral  
PT infection  
PS

XX Example 3; Page 21; 47pp; English.

CC cDNA generated from PMA-stimulated CV-1/EBNA cells was amplified  
CC by PCR using primers (AA084585-87) based on the N-terminal sequence  
CC of simian interleukin-15 (sIL-15). A clone encoding sIL-15 was  
CC obtained (AA084583).

SO Sequence 17 BP; 3 A; 3 C; 2 G; 4 T; 5 other;

Query Match 81.2%; Score 13.8; DB 16; Length 17;  
Best Local Similarity 100.0%; Pred. No. 83;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTCNGAYTCNGTCTTA 17  
|||||  
Db 1 acrtcngaytcngtctta 17

RESULT 3

AAT49458 ID AAT49458 standard; cDNA; 17 BP.

XX AAT49458;

DT 11-MAR-1997 (first entry)

XX Epithelium derived T cell factor PCR primer.

DE Simian epithelium derived T cell factor; sETF; African green monkey;  
KW Cercopithecus aethiops; CV1/EBNA cell; T-cell; lymphocyte;  
KW proliferation; differentiation; gastrointestinal; HIV infection;  
KW human immunodeficiency virus; polymerase chain reaction; ss.

XX Synthetic.

OS US5574138-A.

XX US5574138-A.

XX 12-NOV-1996.

XX 08-MAR-1993; 93US-0031399.

XX 22-FEB-1995; 95US-0393305.

XX 08-MAR-1993; 93US-0031399.

XX 22-APR-1994; 94US-0233606.

XX (IMMV) IMMUNEX CORP.

PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;  
PI Rauch C;  
XX

XX WPI: 1996-517923/51.

PT New epithelium derived T cell factor - induces proliferation of T  
PT and B cells, stimulates destruction of tumour and virus-infected  
PT cells and protects against toxicity, partic. for treating intestinal  
PT disease and HIV infection  
PS

XX Example 3; Column 25; 35pp; English.

CC The simian ETF (epithelium derived T cell factor) was isolated from  
CC African green monkey CV1/EBNA cell conditioned medium. The N-  
CC terminal sequence of the purified sETF was determined and then PCR  
CC primers were designed based on the sequence information. The  
CC present sequence is that of a degenerate primer based on amino acids  
CC 26-31. I.e. Tyr-Phe-Glu-Ser-Asp-Val. A 92 bp fragment was  
CC amplified from CV1/EBNA DNA and was used as a probe to screen a

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 02:20:51 ; Search time 291.55 Seconds  
(without alignments)  
100.112 Million cell updates/sec

Title: US-09-724-841-10

Perfect score: 17  
Sequence: 1 ACRTCCAGATCNGTCTRTA 17

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq Length: 0  
Maximum DB seq Length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

N\_Geneseq\_032802:\*

- 1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*
- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*
- 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*
- 4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*
- 5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*
- 6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*
- 7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*
- 8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*
- 9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*
- 10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*
- 11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*
- 12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*
- 13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*
- 14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*
- 15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*
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- 19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*
- 20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*
- 21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*
- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13.8	81.2	17	16	AAT00529
2	13.8	81.2	17	16	AAQ84586
3	13.8	81.2	17	17	AAT49458
4	13.8	81.2	17	17	AAT42245
5	13.8	81.2	17	19	AAV02876
6	13.8	81.2	17	20	AAZ9484
7	13.8	81.2	17	21	AAZ38247
8	13.8	81.2	17	22	AAE57022
9	13.8	81.2	23	23	AA565068

C 10	13.8	81.2	1140	21	AAC98828	Human pancreatic c
C 11	13.8	81.2	1199	22	AAH01023	Streptococcus pneu
C 12	13.8	81.2	1260	20	AAZ35943	Streptococcus pneu
C 13	13.8	81.2	1260	20	AAZ35944	Streptococcus pneu
C 14	13.8	81.2	1260	20	AAZ35945	Streptococcus pneu
C 15	13.8	81.2	1260	20	AAZ35946	Streptococcus pneu
C 16	13.8	81.2	1260	20	AAZ35947	Streptococcus pneu
C 17	13.8	81.2	1652	21	AAZ3926	Adenyl cyclase C
C 18	13.8	81.2	1835	23	AA565071	DNA encoding novel
C 19	13.8	81.2	2092	17	AA114529	Human adenyl cycl
C 20	13.8	81.2	3343	22	AA160763	Human polynucleot
C 21	13.8	81.2	4008	17	AA114528	Rat adenyl cyclase
C 22	13.8	81.2	4008	17	AAZ3919	Adenyl cyclase t
C 23	13.8	81.2	4011	22	AAZ06820	Human adenylate cy
C 24	13.8	81.2	5717	19	AAV52235	Streptococcus pneu
C 25	12.8	75.3	255	22	AAH82129	Rat differential t
C 26	12.8	75.3	318	22	ABA88626	Escherichia coli p
C 27	12.8	75.3	413	22	ABA07610	Human ovarian and
C 28	12.8	75.3	413	22	AA102192	Human reproductive
C 29	12.8	75.3	1158	21	AAZ07574	Fusarium venenatum
C 30	12.8	75.3	1233	22	AAZ65158	Human immune/haema
C 31	12.8	75.3	1293	22	ABA88809	Escherichia coli p
C 32	12.8	75.3	1378	22	ABA88908	Escherichia coli p
C 33	12.8	75.3	1588	17	AAZ31005	Rat cardiac alpha
C 34	12.8	75.3	1906	19	AAV59637	Human secreted pro
C 35	12.8	75.3	2404	23	AB104507	Drosophila melanog
C 36	12.8	75.3	2436	19	AAV59776	Human secreted pro
C 37	12.8	75.3	2474	21	AAZ94266	Mung bean ACC synt
C 38	12.8	75.3	2483	23	AB127452	Drosophila melanog
C 39	12.8	75.3	3503	23	AB125371	Drosophila melanog
C 40	12.8	75.3	3747	19	AAV05714	Maize retinoblasto
C 41	12.8	75.3	3747	19	AAV17081	Maize retinoblasto
C 42	12.8	75.3	4804	23	AAZ46086	CDNA encoding a re
C 43	12.8	75.3	5166	23	AB104506	Drosophila melanog
C 44	12.8	75.3	8483	23	AB125370	Drosophila melanog
C 45	12.8	75.3	18796	23	AA559517	Propionibacterium

#### ALIGNMENTS

RESULT 1	
ID AAT00529	standard; cDNA; 17 BP.
XX	
AC AAT00529;	
XX	
DT 02-FEB-1996	(first entry)
XX	
DE	Degenerate PCR primer based on simlan IL-15 mature N-terminus 26-31.
XX	
KW	Interleukin-15; epithelium-derived T-cell factor; T lymphocyte;
KM	PCR primer: ss.
XX	
OS	Synthetic.
XX	
FH	Key
FT	misc.feature
FT	Location/Qualifiers
FT	1..17
FT	/*tag= a
FT	/note= "std IUPAC codes used"
PN	
PD	WO9527722-A.
XX	
XX	19-OCT-1995.
XX	
PF	06-APR-1994; 94WO-US03793.
XX	
PR	06-APR-1994; 94WO-US03793.
XX	
PA	(IMMUNEX CORP.
XX	
XX	Anderson DM, Eisenman JR, Fung V, Grabstein KH;
PI	Rauch C;





REFERENCE 2 (sites)  
AUTHORS Asahi, Y. and Ubukata, K.  
TITLE Association of a thr-371 substitution in a conserved amino acid motif of penicillin-binding protein 1A with penicillin resistance of Streptococcus pneumoniae  
JOURNAL Antimicrob. Agents Chemother. 42 (9), 2267-2273 (1998)  
MEDLINE 98409715  
FEATURES  
Source Location/Qualifiers  
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1. 1195  
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/codon\_start=1  
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/db\_xref="GI:3393660"  
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BASE COUNT 379 a 289 c 240 g 266 t 1 others  
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Best Local Similarity 70.6%; Pred. No. 4.9e+02;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 ACRTCGAYTCNGTRTA 17  
11:11 11:11 11:11  
Db 678 ACGTCGATTCGGTATA 662  
RESULT 15  
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LOCUS Streptococcus pneumoniae pbp1a gene for penicillin binding protein  
DEFINITION 1A, partial cds, isolate:#24/TJ25, #26/TJ29.  
ACCESSION AB006879  
VERSION AB006879.1 GI:3395661  
KEYWORDS pbp1a; penicillin binding protein 1A.  
SOURCE Streptococcus pneumoniae (isolate:#24/TJ25, #26/TJ29) DNA.  
ORGANISM Streptococcus pneumoniae  
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
Streptococcus.  
1 (bases 1 to 1195)  
Asahi, Y.  
REFERENCE  
AUTHORS Direct Submission  
TITLE Submitted (27-AUG-1997) Yasuko Asahi, Teikyo University School of  
JOURNAL Medicine, Department of Clinical Pathology; 2-11-1 Kaga,  
MEDLINE Itabashi-ku, Tokyo 173-8605, Japan  
98409715 (E-mail:asahi@med.teikyo-u.ac.jp, Tel:81-3-3964-1211,  
Fax:81-3-3963-6023)  
2 (sites)  
Asahi, Y. and Ubukata, K.  
REFERENCE  
AUTHORS Association of a thr-371 substitution in a conserved amino acid  
TITLE motif of penicillin-binding protein 1A with penicillin resistance  
JOURNAL of Streptococcus pneumoniae  
MEDLINE Antimicrob. Agents Chemother. 42 (9), 2267-2273 (1998)  
98409715  
FEATURES  
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SEKMAAAYAAAFANGSTYKPMYIHKVVSDESEKESVNGTRAKETTAAYMTDMKT  
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BASE COUNT 378 a 292 c 241 g 284 t  
ORIGIN  
Query Match 81.2%; Score 13.8; DB 1; Length 1195;  
Best Local Similarity 70.6%; Pred. No. 4.9e+02;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 ACRTCGAYTCNGTRTA 17  
11:11 11:11 11:11  
Db 678 ACGTCGATTCGGTATA 662

Search completed: June 19, 2002, 02:54:34  
Job time: 7092 sec

## ORIGIN

Query Match 81.2% Score 13.8: DB 1: Length 930;  
 Best Local Similarity 70.6% Pred. No. 4.9e+02;  
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17  
 ||:| | | | | | | | | |  
 Db 708 ACCTCCGATTCCTATA 692

RESULT 12 AF046234 930 bp DNA linear BCT 30-JUN-1998  
 LOCUS Streptococcus pneumoniae strain 56739 penicillin-binding protein 1A  
 DEFINITION (ponA) gene, partial cds.  
 ACCESSION AF046234.1 GI:2911413  
 VERSION AF046234.1  
 KEYWORDS Streptococcus pneumoniae.  
 SOURCE Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 ORGANISM Streptococcus pneumoniae.

REFERENCE 1 (bases 1 to 930)  
 AUTHORS Smith,A.M. and Klugman,K.P.  
 TITLE Alterations in PBP 1A essential for high-level penicillin resistance in Streptococcus pneumoniae  
 JOURNAL Antimicrob. Agents Chemother. 42 (6), 1329-1333 (1998)

MEDLINE 98287565  
 REFERENCE 2 (bases 1 to 930)  
 AUTHORS Smith,A.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-FEB-1998) Microbiology, SAHMR Hospital, Johannesburg, Gauteng 2000, South Africa

## FEATURES

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BASE COUNT 288 a 216 c 196 g 230 t  
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 Best Local Similarity 70.6% Pred. No. 4.9e+02;  
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17  
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 Db 708 ACCTCCGATTCCTATA 692

RESULT 13 AF046236 930 bp DNA linear BCT 30-JUN-1998  
 LOCUS Streptococcus pneumoniae strain N94 penicillin-binding protein 1A  
 DEFINITION

(ponA) gene, partial cds.  
 ACCESSION AF046236 GI:2911417  
 VERSION AF046236.1  
 KEYWORDS Streptococcus pneumoniae.  
 SOURCE Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 ORGANISM Streptococcus pneumoniae.

REFERENCE 1 (bases 1 to 930)  
 AUTHORS Smith,A.M. and Klugman,K.P.  
 TITLE Alterations in PBP 1A essential for high-level penicillin resistance in Streptococcus pneumoniae  
 JOURNAL Antimicrob. Agents Chemother. 42 (6), 1329-1333 (1998)

MEDLINE 98287565  
 REFERENCE 2 (bases 1 to 930)  
 AUTHORS Smith,A.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-FEB-1998) Microbiology, SAHMR Hospital, Johannesburg, Gauteng 2000, South Africa

## FEATURES

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BASE COUNT 287 a 213 c 201 g 229 t  
 ORIGIN

Query Match 81.2% Score 13.8: DB 1: Length 930;  
 Best Local Similarity 70.6% Pred. No. 4.9e+02;  
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17  
 ||:| | | | | | | | | |  
 Db 708 ACCTCCGATTCCTATA 692

RESULT 14 AB006878 1195 bp DNA linear BCT 13-FEB-1999  
 LOCUS Streptococcus pneumoniae pbp1a gene for penicillin binding protein 1A, partial cds. Isolate:#23/HSB21.  
 DEFINITION

ACCESSION AB006878 GI:3395659  
 VERSION AB006878.1  
 KEYWORDS pbp1a; penicillin binding protein 1A.  
 SOURCE Streptococcus pneumoniae (isolate:#23/HSB21) DNA.  
 ORGANISM Streptococcus pneumoniae  
 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;

REFERENCE 1 (bases 1 to 1195)  
 AUTHORS Asahi,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-APR-1997) Yasuko Asahi, Teikyo University School of Medicine, Department of Clinical Pathology, 2-11-1 Kaga, Itabashi-ku, Tokyo 173-8605, Japan  
 (E-mail:asahi.med.teikyo-u.ac.jp, Tel:81-3-3964-1211, Fax:81-3-3963-6023)

CDS	/gene="ponA" <1..>930 /gene="ponA" /note="PBP 1A" /codon_start=1 /transl_table=11 /product="penicillin-binding protein 1A" /protein_id="AAC24697.1" /db_xref="GI:2911410"
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Matches 12: Conservative 3: Mismatches 2: Indels 0: Gaps 0:	
QY 1 ACRTCGAGTCNGTRTA 17	
Dd 708 ACGTCGATTCGGATA 692	
RESULT 11	
AF046233/c	930 bp DNA linear BCT 30-JUN-1998
LOCUS	Streptococcus pneumoniae strain 64429 penicillin-binding protein 1A
DEFINITION	(ponA) gene, partial cds.
ACCESSION	AF046233
VERSION	AF046233.1 GI:2911411
KEYWORDS	
SOURCE	
ORGANISM	Streptococcus pneumoniae. Streptococcus pneumoniae Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
REFERENCE	1 (bases 1 to 930) Smith,A.M. and Klugman,K.P. Alterations in PBP 1A essential for high-level penicillin resistance in Streptococcus pneumoniae Antimicrob. Agents Chemother. 42 (6), 1329-1333 (1998)
JOURNAL MEDLINE REFERENCE	2 (bases 1 to 930) Smith,A.M. Direct Submission Submitted (06-FEB-1998) Microbiology, SAIR Hospital, Johannesburg, JOURNALS Gauteng 2000, South Africa Location/Qualifiers 1..930 /organism="Streptococcus pneumoniae" /strain="64429" /db_xref="taxon:1313" <1..>930 /gene="ponA" <1..>930 /note="PBP 1A" /gene="PBP 1A" /codon_start=1 /transl_table=11 /product="penicillin-binding protein 1A" /protein_id="AAC24697.1" /db_xref="GI:2911412"
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base count	288 a 215 c 198 g 229 t

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ACRTGATCNGTGT 17
Db 1 ACRTGATCNGTGT 17

RESULT 7
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LOCUS Ballochia hildegarde wingless (wg) gene, partial cds.
DEFINITION AF233548
ACCESSION AF233548.2 GI:12863151
KEYWORDS
SOURCE Ballochia hildegarde.
ORGANISM Ballochia hildegarde.
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
Ditrysia; Papilionoidea; Lycaenidae; Poritillinae; Liptenini;
Ballochia.
REFERENCE 1 (bases 1 to 350)
AUTHORS Campbell,D.L., Brower,A.V. and Pierce,N.E.
TITLE Molecular evolution of the wingless gene and its implications for
the phylogenetic placement of the butterfly family Riodinidae
(J Lepidoptera: Papilionoidea)
JOURNAL Mol. Biol. Evol. 17 (5), 684-696 (2000)
MEDLINE 20243641
REFERENCE 2 (bases 1 to 350)
AUTHORS Campbell,D.L., Brower,A.V.Z. and Pierce,N.E.
TITLE Direct Submision
JOURNAL Submitted (11-FEB-2000) Organismic and Evolutionary Biology,
Harvard University, 26 Oxford St., Cambridge, MA 02138, USA
COMMENT On Feb 16, 2001 this sequence version replaced gi:7804846.
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/protein_id="AAF70152.2"
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GCDLMCCGGGFRQ"
BASE COUNT 101 a 78 c 88 g 83 t
ORIGIN
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Best Local Similarity 70.6%; Pred. No. 5e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGATCNGTGT 17
Db 243 ACATCAGACTCGGTATA 259

RESULT 8
AC038651
ID AC038651 standard; DNA; HTG; 850 BP.
XX
AC AC038651;
XX
SV AC038651.1

XX 10-APR-2000 (Rel. 63, Created)
DT 10-APR-2000 (Rel. 63, Last updated, Version 1)
XX
DE Giardia intestinalis clone EJ2784 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
XX
XX HTG; HTGS_PHASE0.
XX
OS Giardia intestinalis
OC Eukaryota; Diplomonadida; Hexamitidae; Giardinales; Giardia.
XX
XX [1]
RN 1-850
RP 1-850
RA Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C.,
RT Hinkle G., Holder M.E., Sogin M.L.;
RL "Giardia: a model for ancient eukaryotic genome analysis";
XX unpublished.
XX
XX [2]
RN 1-850
RP 1-850
RA Eakin N.Q., Morrison H.G., McArthur A.G., Nixon J., Kim U., Crocker M.C.,
RT Hinkle G., Holder M.E., Sogin M.L.;
RL Submitted (10-APR-2000) to the EMBL/GenBank/DBJ databases.
XX Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
XX Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
XX
XX * NOTE: This record contains 1 individual
XX * sequencing reads that have not been assembled into
XX * contigs. Runs of N are used to separate the reads
XX * and the order in which they appear is completely
XX * arbitrary. Low-pass sequence sampling is useful for
XX * identifying clones that may be gene-rich and allows
XX * overlap relationships among clones to be deduced.
XX * However, it should not be assumed that this clone
XX * will be sequenced to completion. In the event that
XX * the record is updated, the accession number will
XX * be preserved.
XX 1
XX 850: contig of 850 bp in length.
XX
XX Key Location/Qualifiers
FH 1..850
FT source /db_xref="taxon:5741"
FT /organism="Giardia intestinalis"
FT /strain="WB-C6"
FT /clone="EJ2784"
XX
XX Sequence 850 BP; 202 A; 207 C; 210 G; 226 T; 5 other;
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Query Match      81.2%; Score 13.8; DB 33; Length 850;
Best Local Similarity 70.6%; Pred. No. 4.9e+02;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ACRTGATCNGTGT 17
Db 819 ACATCAGATTCGGTATA 835

RESULT 9
AF046231 930 bp DNA linear BCT 30-JUN-1998
LOCUS Streptococcus pneumoniae strain 65654 penicillin-binding protein 1A
DEFINITION (pna) gene, partial cds.
ACCESSION AF046231
VERSION AF046231.1 GI:2911407
KEYWORDS
SOURCE Streptococcus pneumoniae.
ORGANISM Streptococcus pneumoniae
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Streptococcus.
REFERENCE 1 (bases 1 to 930)
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17  
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Db 1 ACRTGNGAYTCNGTRTA 17

RESULT 2  
LOCUS AR070286 17 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 10 from patent US 5892001.  
ACCESSION AR070286  
VERSION AR070286.1 GI:7221174  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Epithelium-derived T-cell factor antibodies  
JOURNAL Patent: US 5892001-A 10 06-APR-1999;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"

BASE COUNT 3 a 3 c 2 g 4 t 5 others

ORIGIN

Query Match 81.2%; Score 13.8; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17  
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Db 1 ACRTGNGAYTCNGTRTA 17

RESULT 3  
LOCUS AR085745 17 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 10 from patent US 5985262.  
ACCESSION AR085745  
VERSION AR085745.1 GI:10012511  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Method of treatment with epithelium derived T-cell factor  
JOURNAL Patent: US 5985262-A 10 16-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"

BASE COUNT 3 a 3 c 2 g 4 t 5 others

ORIGIN

Query Match 81.2%; Score 13.8; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17  
|||||

Db 1 ACRTGNGAYTCNGTRTA 17

RESULT 4  
LOCUS 125787 17 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 10 from patent US 5552303.  
ACCESSION 125787  
VERSION 125787.1 GI:1605657

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grabstein,K.H., Anderson,D., Eisenman,J., Fung,V. and Rauch,C.  
TITLE DNA encoding epithelium-derived T-cell factor  
JOURNAL Patent: US 5552303-A 10 03-SEP-1996;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"

BASE COUNT 3 a 3 c 2 g 4 t 5 others

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17  
|||||

Db 1 ACRTGNGAYTCNGTRTA 17

RESULT 5  
LOCUS 128854 17 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 10 from patent US 5574138.  
ACCESSION 128854  
VERSION 128854.1 GI:1819636  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Epithelium-derived T-cell factor  
JOURNAL Patent: US 5574138-A 10 12-NOV-1996;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"

BASE COUNT 3 a 3 c 2 g 4 t 5 others

ORIGIN

Query Match 81.2%; Score 13.8; DB 6; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACRTGNGAYTCNGTRTA 17  
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Db 1 ACRTGNGAYTCNGTRTA 17

RESULT 6  
LOCUS 179224 17 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 10 from patent US 5707616.  
ACCESSION 179224  
VERSION 179224.1 GI:3207514  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.  
TITLE Method for treating or preventing gastrointestinal disease with  
epithelium-derived T-cell factor  
JOURNAL Patent: US 5707616-A 10 13-JUN-1998;  
FEATURES Location/Qualifiers  
source 1..17  
/organism="unknown"

BASE COUNT 3 a 3 c 2 g 4 t 5 others

1	13.8	81.2	17	6	AR004272
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3	13.8	81.2	17	6	AR085745 Sequence
4	13.8	81.2	17	6	125787 Sequence 10
5	13.8	81.2	17	6	128854 Sequence 10
6	13.8	81.2	17	6	179224 Sequence 10
7	13.8	81.2	350	33	AF233548 Balclochl
8	13.8	81.2	850	33	AF233548 Balclochl
9	13.8	81.2	930	1	AC038651 Giardia 1
10	13.8	81.2	930	1	AF046231 Streptoco
11	13.8	81.2	930	1	AF046232 Streptoco
12	13.8	81.2	930	1	AF046233 Streptoco
13	13.8	81.2	930	1	AF046234 Streptoco
14	13.8	81.2	930	1	AF046236 Streptoco
15	13.8	81.2	1195	1	AB006878 Streptoco
16	13.8	81.2	1195	6	AX110281 Sequence
17	13.8	81.2	1652	6	AR106662 Sequence
18	13.8	81.2	1783	9	AF070583 Homo sapl
19	13.8	81.2	2092	9	HUMADNXY
20	13.8	81.2	2110	9	HSADPYCL
21	13.8	81.2	2160	1	AF210752 Streptoco
22	13.8	81.2	2784	9	HSMB00114 Homo sapl
23	13.8	81.2	4008	6	AR106655 Sequence
24	13.8	81.2	4008	10	RATADNXYIT
25	13.8	81.2	4728	8	BF294841 Polynasid
26	13.8	81.2	5717	6	BD003782 Homo sapl
27	13.8	81.2	5873	9	AB028983 Homo sapl
28	13.8	81.2	7058	9	AP000930 Homo sapl
29	13.8	81.2	11735	1	AE007378 Streptoco
30	13.8	81.2	50485	5	AC082648 Homo sapl
31	13.8	81.2	65028	2	AC103422 Rattus no
32	13.8	81.2	109626	2	AC010346 Homo sapl
33	13.8	81.2	110000	2	AL6056502
34	13.8	81.2	122717	2	AF0001186 Continuation (3 of
35	13.8	81.2	130977	2	AP002347 Homo sapl
36	13.8	81.2	137296	2	AC093244 Homo sapl
37	13.8	81.2	145035	2	CNS072EY AL450442 Human chr
38	13.8	81.2	145785	2	AC016173 Homo sapl
39	13.8	81.2	145868	2	AC016802 Homo sapl
40	13.8	81.2	157848	2	AC079763 Homo sapl
41	13.8	81.2	158758	9	AC093591 Homo sapl
42	13.8	81.2	163009	9	AC011884 Homo sapl
43	13.8	81.2	163811	2	AC025891 Homo sapl
44	13.8	81.2	167337	9	AC021609 Homo sapl
45	13.8	81.2	167642	9	CNS07ECT AL442163 Human chr



ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,317B  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 69 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
US-08-392-317B-9

Query Match 80.0%; Score 14.4; DB 1; Length 69;  
Best Local Similarity 72.2%; Pred. No. 8.3;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Caps 0;  
OY 1 AAYTGGTNAAGTNAATH 18  
Db 49 AACTGGCTGATCTAATA 66

Search completed: June 19, 2002, 02:22:11  
Job time: 5419 sec

INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
US-09-134-134A-7

Query Match 80.0%; Score 14.4; DB 4; Length 39;  
Best Local Similarity 72.2%; Pred. No. 7.6;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGTNAAYGTNATH 18  
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DB 22 AACTGGTGATGTATA 39

RESULT 13  
US-09-134-456-7  
Sequence 7, Application US/09134456  
Patent No. 6168783  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Paxton, Raymond  
APPLICANT: Pettit, Dean  
TITLE OF INVENTION: Antagonists of IL-15  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,456  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/392,317  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
US-09-134-456-7

Query Match 80.0%; Score 14.4; DB 4; Length 39;  
Best Local Similarity 72.2%; Pred. No. 7.6;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGTNAAYGTNATH 18  
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DB 22 AACTGGTGATGTATA 39

RESULT 14  
US-09-196-427-7  
Sequence 7, Application US/09196427  
Patent No. 6177079  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Paxton, Raymond  
APPLICANT: Pettit, Dean  
TITLE OF INVENTION: Antagonists of IL-15  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: Patentin Release #1.0, Version #1.25  
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FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/392,317  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
US-09-196-427-7

Query Match 80.0%; Score 14.4; DB 4; Length 39;  
Best Local Similarity 72.2%; Pred. No. 7.6;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGTNAAYGTNATH 18  
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DB 22 AACTGGTGATGTATA 39

RESULT 15  
US-08-392-317B-9  
Sequence 9, Application US/08392317B  
Patent No. 5795966  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Paxton, Raymond  
APPLICANT: Pettit, Dean  
TITLE OF INVENTION: Antagonists of IL-15  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA

Db 8 AACTGGGTGAATCTATA 25

RESULT 10  
US-08-392-317B-7  
Sequence 7, Application US/08392317B  
Patent No. 5795966  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Paxton, Raymond  
TITLE OF INVENTION: Antagonists of IL-15  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/392,317B  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
US-08-392-317B-7

Query Match 80.0%; Score 14.4; DB 1; Length 39;  
Best Local Similarity 72.2%; Pred. No. 7.6;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18  
||:||||| ||:|||||  
Db 22 AACTGGGTGAATCTATA 39

RESULT 11  
US-09-134-132-7  
Sequence 7, Application US/09134132  
Patent No. 6013480  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Paxton, Raymond  
TITLE OF INVENTION: Antagonists of IL-15  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,132  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: US/08/392,317  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
US-09-134-132-7

Query Match 80.0%; Score 14.4; DB 3; Length 39;  
Best Local Similarity 72.2%; Pred. No. 7.6;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18  
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Db 22 AACTGGGTGAATCTATA 39

RESULT 12  
US-09-134-134A-7  
Sequence 7, Application US/09134134A  
Patent No. 6165466  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Paxton, Raymond  
TITLE OF INVENTION: Antagonists of IL-15  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: Word for Windows 95, 7.0  
SOFTWARE: Patentln Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/134,134A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: 08/392,317  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2831  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/189,193  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-189-193-9

Query Match 80.0%; Score 14.4; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18  
DB 1 AAYTGGTNAAYGTNATH 18

RESULT 8  
PCT-US94-03793-9  
GENERAL INFORMATION:  
APPLICANT: Grabstejn, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eissenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: Interleukin-15  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/03793  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Launer, Charlene  
REGISTRATION NUMBER: 33,035

REFERENCE/DOCKET NUMBER: 2811  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PCT-US94-03793-9

Query Match 80.0%; Score 14.4; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18  
DB 1 AAYTGGTNAAYGTNATH 18

RESULT 9  
US-08-842-947-1  
Sequence 1, Application US/08842947  
Patent No. 6001973  
GENERAL INFORMATION:  
APPLICANT: Strom, Terry B.  
APPLICANT: Maslinski, Wlodzislaw  
TITLE OF INVENTION: ANTAGONISTS OF INTERLEUKIN-15  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/842,947  
FILING DATE: 25-APR-1997  
CLASSIFICATION: 432  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/016,634  
FILING DATE: 26-APR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 01948/039001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-842-947-1

Query Match 80.0%; Score 14.4; DB 3; Length 25;  
Best Local Similarity 72.2%; Pred. No. 7.1;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18

REFERENCE/DOCKET NUMBER: 2811  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0430  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-08-504-042-9

Query Match 80.0%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 AAYTGGTNAAYGTNATH 18  
|||||  
Db 1 AAYTGGTNAAYGTNATH 18

RESULT 5  
US-08-725-969-9  
Sequence 9, Application US/08725969  
Patent No. 5892001  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
City: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/725,969  
FILING DATE: 04-OCT-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-725-969-9

Query Match 80.0%; Score 14.4; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 AAYTGGTNAAYGTNATH 18  
|||||  
Db 1 AAYTGGTNAAYGTNATH 18

RESULT 6  
US-08-794-524-9  
Sequence 9, Application US/08794524  
Patent No. 5985262  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Seed and Berry  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
City: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/794,524  
FILING DATE: 03-FEB-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/393,305  
FILING DATE: 22-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Mcmasters, David D.  
REGISTRATION NUMBER: 33,963  
REFERENCE/DOCKET NUMBER: 480052.409C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-622-4900  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-794-524-9

Query Match 80.0%; Score 14.4; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 AAYTGGTNAAYGTNATH 18  
|||||  
Db 1 AAYTGGTNAAYGTNATH 18

RESULT 7  
US-09-189-193-9  
Sequence 9, Application US/09189193  
Patent No. 6184359  
GENERAL INFORMATION:  
APPLICANT: Grabstein, Kenneth  
APPLICANT: Anderson, Dirk  
APPLICANT: Eisenman, June  
APPLICANT: Fung, Victor  
APPLICANT: Rauch, Charles  
TITLE OF INVENTION: EPITHELUM-DERIVED T-CELL FACTOR  
NUMBER OF SEQUENCES: 15



QY 1 AAYTGGGTAAAGTATNATH 18  
|||||

Db 1 AAYTGGGTAAAGTATNATH 18

## RESULT 2

US-08-393-305-9

; Sequence 9, Application US/08393305  
; Patent No. 5574138

## GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

APPLICANT: Anderson, Dirk

APPLICANT: Eisenman, June

APPLICANT: Fung, Victor

APPLICANT: Rauch, Charles

TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR

NUMBER OF SEQUENCES: 15

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/393,305

FILING DATE: 22-FEB-1995

## CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: McMaisters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 480052.409C2

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

## INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-393-305-9

QY 1 AAYTGGGTAAAGTATNATH 18  
|||||

Db 1 AAYTGGGTAAAGTATNATH 18

Query Match 80.0%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.7;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 3

US-08-726-817-9

; Sequence 9, Application US/08726817  
; Patent No. 5707616

## GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

APPLICANT: Anderson, Dirk

APPLICANT: Eisenman, June

APPLICANT: Fung, Victor

TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR

NUMBER OF SEQUENCES: 15

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,817

FILING DATE: 04-OCT-1996

## CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/393,305

FILING DATE: 22-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: McMaisters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 480052.409C2

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

## INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-726-817-9

QY 1 AAYTGGGTAAAGTATNATH 18  
|||||

Db 1 AAYTGGGTAAAGTATNATH 18

Query Match 80.0%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## RESULT 4

US-08-504-042-9

; Sequence 9, Application US/08504042  
; Patent No. 5747024

## GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

APPLICANT: Anderson, Dirk

APPLICANT: Eisenman, June

APPLICANT: Fung, Victor

APPLICANT: Rauch, Charles

TITLE OF INVENTION: Epithelial-derived T-cell Factor

NUMBER OF SEQUENCES: 12

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/504,042

FILING DATE: 19-JUL-1995

## CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/031,399

FILING DATE: 08-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Launer, Charlene

REGISTRATION NUMBER: 33,035

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:51:52 ; Search time 66.01 Seconds  
(without alignments)  
66.981 Million cell updates/sec

Title: US-09-724-841-9

Perfect score: 18

Sequence: 1 AAYTGCTMAAYGTNATH 18

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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4: /cgcn2\_6/ptodata/2/lna/5B\_COMB.seq:\*  
5: /cgcn2\_6/ptodata/2/lna/5A\_COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	14.4	80.0	18	1	US-08-393-305-9
3	14.4	80.0	18	1	US-08-726-817-9
4	14.4	80.0	18	1	US-08-504-042-9
5	14.4	80.0	18	2	US-08-725-969-9
6	14.4	80.0	18	2	US-08-794-524-9
7	14.4	80.0	18	4	US-09-189-193-9
8	14.4	80.0	18	5	PCT-US94-03793-9
9	14.4	80.0	25	3	US-08-842-847-1
10	14.4	80.0	39	1	US-08-392-317B-7
11	14.4	80.0	39	3	US-09-134-132-7
12	14.4	80.0	39	4	US-09-134-134A-7
13	14.4	80.0	39	4	US-09-134-134A-7
14	14.4	80.0	39	4	US-09-196-427-7
15	14.4	80.0	69	3	US-08-392-317B-9
16	14.4	80.0	69	3	US-09-134-132-9
17	14.4	80.0	69	4	US-09-134-134A-9
18	14.4	80.0	69	4	US-09-134-134A-9
19	14.4	80.0	69	4	US-09-196-427-9
20	14.4	80.0	345	1	US-08-393-305-12
21	14.4	80.0	345	1	US-08-393-305-13
22	14.4	80.0	345	1	US-08-726-817-12
23	14.4	80.0	345	1	US-08-726-817-13
24	14.4	80.0	345	2	US-08-725-969-12
25	14.4	80.0	345	2	US-08-725-969-13
26	14.4	80.0	345	2	US-08-794-524-12
27	14.4	80.0	345	2	US-08-794-524-13

#### ALIGNMENTS

28	14.4	80.0	345	4	US-09-189-193-12	Sequence 12, Appl
29	14.4	80.0	345	4	US-09-189-193-13	Sequence 13, Appl
30	14.4	80.0	489	1	US-08-031-399-1	Sequence 1, Appl1
31	14.4	80.0	489	1	US-08-031-399-4	Sequence 4, Appl1
32	14.4	80.0	489	1	US-08-393-305-1	Sequence 1, Appl1
33	14.4	80.0	489	1	US-08-393-305-4	Sequence 4, Appl1
34	14.4	80.0	489	1	US-08-335-733-1	Sequence 1, Appl1
35	14.4	80.0	489	1	US-08-726-817-1	Sequence 1, Appl1
36	14.4	80.0	489	1	US-08-726-817-4	Sequence 4, Appl1
37	14.4	80.0	489	1	US-08-504-042-1	Sequence 1, Appl1
38	14.4	80.0	489	1	US-08-504-042-4	Sequence 4, Appl1
39	14.4	80.0	489	1	US-08-392-317B-1	Sequence 1, Appl1
40	14.4	80.0	489	1	US-08-392-317B-2	Sequence 2, Appl1
41	14.4	80.0	489	2	US-08-725-969-1	Sequence 1, Appl1
42	14.4	80.0	489	2	US-08-725-969-4	Sequence 4, Appl1
43	14.4	80.0	489	2	US-08-794-524-1	Sequence 1, Appl1
44	14.4	80.0	489	2	US-08-794-524-4	Sequence 4, Appl1
45	14.4	80.0	489	3	US-08-842-847-5	Sequence 5, Appl1

RESULT 1  
US-08-031-399-9

Sequence 9, Application US/08031399

Patent No. 5552303

GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

APPLICANT: Anderson, Dirk

APPLICANT: Eisenman, June

APPLICANT: Rauch, Victor

TITLE OF INVENTION: Epithelium-derived T-cell factor

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/031.399

FILING DATE: 19930308

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Launer, Charlene

REGISTRATION NUMBER: 33,035

REFERENCE/DOCKET NUMBER: 2811

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0430

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-031-399-9

Query Match 80.0%; Score 14.4; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



RESULT 14  
 LOCUS AO329420 654 bp DNA linear GSS 08-JAN-1999  
 DEFINITION nbxb0044p20f CUGI Rice BAC library Oryza sativa genomic clone  
 ACCESSION AO329420  
 VERSION AO329420.1 GI:4121270  
 KEYWORDS GSS.  
 SOURCE Oryza sativa.  
 ORGANISM Oryza sativa.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 654)  
 AUTHORS Wing, R.A. and Dean, R.A.  
 TITLE A BAC End Sequencing Framework to Sequence the Rice Genome  
 JOURNAL Unpublished (1998)  
 COMMENT Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Seq primer: TTAATACGACTCACTATAGG  
 Class: BAC ends  
 High quality sequence stop: 254.  
 Location/Qualifiers  
 1..654  
 /organism="Oryza sativa"  
 /strain="Japanica"  
 /cultivar="Nipponbare"  
 /db\_xref="taxon:4330"  
 /clone="nbxb0044p20f"  
 /clone\_lib="CUGI Rice BAC Library"  
 /tissue\_type="Leaf"  
 /lab\_host="E. coli DH10B"  
 /note="Vector: pBeloBAC11. Site\_1: HindIII; Site\_2:  
 HindIII; Rice is one of two most popular grains in the  
 world. Half of the world population especially those  
 inhabiting highly populated areas of the humid tropics  
 and subtropics, rely on rice as their primary source of  
 carbohydrate. Monocotyledonous rice is a diploid plant  
 (2n=24) with a haploid genome equivalent of 431 Mbp  
 (Arumuganathan and Earle, 1991). The relatively small  
 genome of rice, three times larger than that of  
 Arabidopsis, makes it suitable for genomic studies. In  
 order to facilitate positional cloning, physical mapping  
 and genome sequencing of rice, we have constructed a BAC  
 library from Oryza sativa, Nipponbare variety. The  
 library contains 36,864 clones with an average insert size  
 of 128.5 Kb providing 10.9 haploid genome equivalents. The  
 deep coverage allows the isolation a particular sequence  
 with a probability of 99.9%. Two high density filters,  
 each containing 18,432 clones (doubly spotted), represent  
 the whole library for colony screening."

BASE COUNT 190 a 83 c 100 g 275 t 6 others  
 ORIGIN

Query Match 80.0%; Score 14.4; DB 12; Length 654;  
 Best Local Similarity 72.2%; Pred. No. 1.8e+03;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGGTNAAYGTNATH 18  
 ||:||||| ||:|||||  
 Db 504 AATTGGCTAATGTAATT 521

RESULT 15  
 LOCUS BF645513/c 674 bp mRNA linear EST 20-DEC-2000

DEFINITION NF020F02EC1F1026 Elicited cell culture Medicago truncatula cDNA  
 clone NF020F02EC 5', mRNA sequence.  
 ACCESSION BF645513  
 VERSION BF645513.1 GI:11910642  
 KEYWORDS EST.  
 SOURCE barrel medic.  
 ORGANISM Medicago truncatula  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;  
 Medicago.  
 REFERENCE 1 (bases 1 to 674)  
 AUTHORS Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,  
 Flores, H.R., Inman, J.T., Weller, J.M. and May, G.D.  
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation -  
 Center for Medicago Genomics Research  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Dixon RA  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
 Tel: 580 221 7302  
 Fax: 580 221 7380  
 Email: radixon@noble.org  
 Insert Length: 674 Std Error: 0.00  
 Plate: 020 row: F column: 02  
 Seq primer: TCACACGAGAACGCTATGAC.  
 Location/Qualifiers  
 1..674  
 /organism="Medicago truncatula"  
 /db\_xref="taxon:3880"  
 /clone="NF020F02EC"  
 /clone\_lib="Elicited cell culture"  
 /tissue\_type="Cell cultures derived from root tissues"  
 /dev\_stage="Cell suspensions were subcultured every 14  
 days. Cells were induced six days after subculture"  
 /note="Vector: Lambda Zap; Cells were induced with yeast  
 cell wall extracts equivalent to 50ug/ml glucose in the  
 final concentration. Samples were taken at 0.5, 1, 12 and  
 24 hours after induction. Equal amounts of RNA from each  
 time point were pooled and used for mRNA isolation."

BASE COUNT 181 a 165 c 122 g 205 t 1 others  
 ORIGIN

Query Match 80.0%; Score 14.4; DB 10; Length 674;  
 Best Local Similarity 72.2%; Pred. No. 1.9e+03;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGGTNAAYGTNATH 18  
 ||:||||| ||:|||||  
 Db 125 AATTGGCTGAACGTGATT 108

Search completed: June 19, 2002, 02:15:49  
 Job time: 7362 sec

using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

BASE COUNT 171 a 106 c 119 g 188 t  
ORIGIN

Query Match 80.0%; Score 14.4; DB 10; Length 584;  
Best Local Similarity 72.2%; Pred. No. 1.8e+03;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGTAAAGTAAATG 18  
||:||||| ||:| ||:  
Db 513 AACTGGTCAATGATC 496

RESULT 12  
LOCUS A0947440 600 bp DNA linear GSS 27-JAN-2000  
DEFINITION Sheared DNA-49K15.TF Sheared DNA Trypanosoma brucei genomic clone  
ACCESSION A0947440  
VERSION A0947440.1 GI:6770705  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei.  
ORGANISM Trypanosoma brucei  
Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE 1 (bases 1 to 600)  
AUTHORS El-Sayed, N., Zhao, H., Gill, S., Sub, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.  
Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library  
Unpublished (1999)  
Other\_GSSs: Sheared DNA-49K15.TF  
Contact: Najib M. El-Sayed  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: nelsayed@tigr.org

TITLE Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page: <http://www.tigr.org/tldb/mdb/tldb/>.  
Seq primer: M13-Forward  
Class: Shotgun.

FEATURES  
SOURCE Location/Qualifiers  
1..600  
/organism="Trypanosoma brucei"  
/strain="TREU927/4 GUTat 10.1"  
/db\_xref="taxon:5691"  
/clone="Sheared DNA-49K15"  
/clone\_lib="Sheared DNA"  
/note="Vector: pUC18; Site\_1: SmaI; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrell, Oxford University Press, 1999)."

BASE COUNT 199 a 127 c 107 g 167 t  
ORIGIN

Query Match 80.0%; Score 14.4; DB 12; Length 600;  
Best Local Similarity 72.2%; Pred. No. 1.8e+03;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGTAAAGTAAATG 18  
||:||||| ||:| ||:  
Db 66 AAYTGGTCAAGTAAAT 83

RESULT 13  
LOCUS BH098364 609 bp DNA linear GSS 19-JUL-2001  
DEFINITION RPCI-24-315N8.TJ RPCI-24 Mus musculus genomic clone RPCI-24-315N8, DNA sequence.  
ACCESSION BH098364  
VERSION BH098364.1 GI:14920086  
KEYWORDS GSS.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 609)  
AUTHORS Zhao, S., Niernan, W., Malek, J., Shatsman, S., Akiner, B., Levins, M., Tsagaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E., Russell, D., de Jong, P. and Fraser, C.M.  
Mouse BAC End Sequences from library RPCI-24  
Unpublished (1999)  
Other\_GSSs: RPCI-24-315N8.TJ  
Contact: Shanying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

TITLE Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong ([pdjong@mail.chu.org](mailto:pdjong@mail.chu.org)). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/orderingframe.html>). BAC end page: [http://www.tigr.org/tldb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tldb/bac_ends/mouse/bac_end_intro.html)  
Plate: 315 row: N column: 8  
Seq primer: SP6  
Class: BAC ends.

FEATURES  
SOURCE Location/Qualifiers  
1..609  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-24-315N8"  
/clone\_lib="RPCI-24"  
/sex="Male"  
/cell\_type="Spleen/Brain"  
/note="Vector: pPARBAC1; Site\_1: BamHI; Site\_2: BamHI; RPCI-24 Mouse BAC library produced by Pieter de Jong. The library was cloned in the pPARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."

BASE COUNT 229 a 100 c 122 g 158 t  
ORIGIN

Query Match 80.0%; Score 14.4; DB 12; Length 609;  
Best Local Similarity 72.2%; Pred. No. 1.8e+03;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 AAYTGGTAAAGTAAATG 18  
||:||||| ||:| ||:  
Db 558 AAYTGGTAAAGTAAAT 575

/note="Vector: pSPORI1. Site.1: SalI; Site.2: NotI. This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT) )-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo

NbHPU, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

BASE COUNT 149 a 91 c 108 g 161 t

Query Match 80.0%; Score 14.4; DB 9; Length 509;  
Best Local Similarity 72.2%; Pred. No. 1.7e+03;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18  
||:||||| ||:| ||:  
DB 249 AACTGGTGACGTATATA 266

RESULT 7  
BF650545/c 515 bp mRNA linear EST 20-DEC-2000  
LOCUS NF09001EC1F1013 Elicited cell culture Medicago truncatula cDNA  
DEFINITION clone NF090F01EC 5', mRNA sequence.  
ACCESSION BF650545  
VERSION BF650545.1 GI:11915675  
KEYWORDS EST.  
SOURCE barrel medic.  
ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

1 (bases 1 to 515)  
Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research  
Unpublished (2000)  
Contact: Dixon RA  
Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73402, USA  
Tel: 580 221 7302  
Fax: 580 221 7380

Email: radixon@noble.org  
Insert length: 515 Std Error: 0.00  
Plate: 090 row: F column: 01  
Seq primer: TCACACAGGAACACGCTATGAC.

FEATURES  
Location/Qualifiers

1..515

/organism="Medicago truncatula"  
/db\_xref="taxon:3880"  
/clone="NF090F01EC"

/clone\_lib="Elicited cell culture"

/tissue\_type="Cell cultures derived from root tissues"

/dev\_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture"

/note="Vector: Lambda zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."

BASE COUNT 135 a 135 c 88 g 157 t

ORIGIN

Query Match 80.0%; Score 14.4; DB 10; Length 515;  
Best Local Similarity 72.2%; Pred. No. 1.7e+03;

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18

DB 124 AAYTGGTGACGTATATT 107  
||:||||| ||:| ||:  
LOCUS TA241H020/c

DEFINITION T. brucei sheared genomic DNA clone 241h02, reverse sequence, genomic survey sequence.  
547 bp DNA linear GSS 13-DEC-2000

ACCESSION AL482700.1 GI:11848562

VERSION AL482700

KEYWORDS GSS.

SOURCE Trypanosoma brucei.

ORGANISM Trypanosoma brucei

Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at <http://www.sanger.ac.uk/projects/T-brucei/>.

FEATURES

source

1..547

/organism="Trypanosoma brucei"

/strain="TREU927"

/db\_xref="taxon:5691"

/clone="241h02"

BASE COUNT 148 a 104 c 105 g 190 t

ORIGIN

Query Match 80.0%; Score 14.4; DB 12; Length 547;  
Best Local Similarity 72.2%; Pred. No. 1.8e+03;  
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAYTGGTNAAYGTNATH 18  
||:||||| ||:| ||:  
DB 475 AAYTGGTGACGTATATA 458

RESULT 9  
AM688129/c 560 bp mRNA linear EST 15-JUN-2000  
LOCUS NF002F06ST 5', mRNA sequence.

DEFINITION NF002F06ST 5', mRNA sequence.

ACCESSION AM688129

VERSION AM688129

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.

1 (bases 1 to 560)

AUTHORS

He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., May, G.D. and Dixon

ACCESSION A0154673 GI:3547343  
 VERSION A0154673.1  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 487)  
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
 Hood,L.  
 TITLE Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
 MEDLINE 99380589  
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Sequence Tagged Connector  
 Plate: 3021 row: E Column: 15  
 Class: BAC ends  
 High quality sequence stop: 487.  
 Location/Qualifiers  
 1..487  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="CIT Approved Human Genomic Sperm Library D"  
 /sex="male"  
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in  
 E-Coli DH10B"  
 BASE COUNT 111 a 136 c 112 g 126 t 2 others  
 ORIGIN  
 Query Match 80.0%; Score 14.4; DB 12; Length 487;  
 Best Local Similarity 72.2%; Pred. No. 1.7e+03;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 AAYTGGTNAAGTGNATH 18  
 ||:||||| ||:|||||  
 Db 66 AATTGGTTATGTCATT 49  
 RESULT 5  
 LOCUS A0132420 490 bp DNA linear GSS 23-SEP-1998  
 DEFINITION HS\_3021\_A1\_C08\_MR CIT Approved Human Genomic Sperm Library D Homo  
 sapiens genomic clone plate=3021 Col=15 Row=E, DNA sequence.  
 ACCESSION A0132420  
 VERSION A0132420.1 GI:3509586  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 490)  
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
 Hood,L.  
 TITLE Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
 MEDLINE 99380589  
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618

Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Sequence Tagged Connector  
 Plate: 3021 row: E Column: 15  
 Class: BAC ends  
 High quality sequence stop: 490.  
 Location/Qualifiers  
 1..490  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="CIT Approved Human Genomic Sperm Library D"  
 /sex="male"  
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in  
 E-Coli DH10B"  
 BASE COUNT 110 a 136 c 113 g 130 t 1 others  
 ORIGIN  
 Query Match 80.0%; Score 14.4; DB 12; Length 490;  
 Best Local Similarity 72.2%; Pred. No. 1.7e+03;  
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 AAYTGGTNAAGTGNATH 18  
 ||:||||| ||:|||||  
 Db 88 AATTGGTNAAGTGCATT 71  
 RESULT 6  
 LOCUS AA463370 509 bp mRNA linear EST 10-JUN-1997  
 DEFINITION zx97412.r1 Soares\_NhHMPU.S1 Homo sapiens cDNA clone IMAGE:811703 5'  
 similar to SW:IL15\_HUMAN P40933 INTERLEUKIN-15 PRECURSOR; mRNA  
 sequence.  
 ACCESSION AA463370  
 VERSION AA463370.1 GI:2188254  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 509)  
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Gelsel,G., Jost,S.,  
 Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.,  
 Schellenberg,K., Steptoe,M., Tan,F., Theisling,B., White,Y., Wyllie,  
 T., Waterston,K. and Wilson,R.  
 Washu-Merck EST Project 1997  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Possible reversed clone: similarity on wrong strand  
 Seq primer: -28m13 rev2 ET from Amersham  
 High quality sequence stop: 416.  
 Location/Qualifiers  
 1..509  
 /organism="Homo sapiens"  
 /db\_xref="GDB:6042614"  
 /db\_xref="taxon:9606"  
 /clone\_lib="IMAGE:811703"  
 /clone\_lib="Soares\_NhHMPU.S1"  
 /tissue\_type="Pooled human melanocyte, fetal heart, and  
 pregnant uterus"  
 /lab\_host="DH10B"  
 /note="Organ: mixed (see below); Vector: pT73D-Pac  
 (pharmacia) with a modified polylinker; Site:1; Not I;  
 Site:2; Eco RI; Equal amounts of plasmid DNA from three  
 normalized libraries (melanocyte 2NBHM, pregnant uterus



```

/clone_lib="OR0030"
/dev_stage="Adult"
/note="Organ: ovary; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT      73 a      32 g      44 t
ORIGIN
Query Match      80.0%; Score 14.4; DB 9; Length 174;
Best Local Similarity 72.2%; Pred. No. 1.3e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY      1 AAYTGGGTAAATGATNATH 18
      11:|||||11:||||11:
Db      145 AATTGGTTAATGTCATT 128

RESULT 2
BE315807/c      359 bp      mRNA      linear      EST 21-DEC-2000
DEFINITION      NF027F03JF1027 Developing leaf Medicago truncatula cDNA clone
LOCUS           NF027F03JF 5', mRNA sequence.
ACCESSION       BE315807
VERSION         BE315807.2 GI:11961409
KEYWORDS        EST.
SOURCE          barrel medic.
ORGANISM        Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;
Medicago.
1 (bases 1 to 359)
Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula leaf library
Unpublished (2000)
On Jul 14, 2000 this sequence version replaced gi:1919584.
JOURNAL
COMMENT          Contact: May GD
                  Plant Biology Division
                  The Samuel Roberts Noble Foundation
                  2510 Sam Noble Parkway, Ardmore, OK 73402, USA
                  Tel: 580 221 7391
                  Fax: 580 221 7380
                  Email: gdmay@noble.org
                  Medicago Genome Initiative accession: MGI:S:16165
                  Insert length: 688 Std Error: 0.00
                  Plate: 027 row: F column: 03
                  Seq primer: TCACACAGAAACGCTATGAC.
FEATURES
source          Location/Qualifiers
                  1..359
                  /organism="Medicago truncatula"
                  /db_xref="taxon:3880"
                  /clone="NF027F03JF"
                  /clone_lib="Developing leaf"
                  /tissue_type="leaf"
                  /dev_stage="Pooled developmental"
                  /note="Vector: lambda zap; Contains a mixture of very
                  young, developing, mature and senescing leaves."
BASE COUNT      91 a      102 c      52 g      114 t
ORIGIN
Query Match      80.0%; Score 14.4; DB 10; Length 359;
Best Local Similarity 72.2%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY      1 AAYTGGGTAAATGATNATH 18

```

```

Db      145 AATTGGGTGAACGTGATT 128
||||| ||||| ||||| |||
RESULT  3
R08151/c
LOCUS   yf17n09.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone.
DEFINITION IMAGE:127169 3, mRNA sequence.
ACCESSION R08151
VERSION   R08151.1 GI:760074
KEYWORDS EST.
SOURCE    human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 380)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
-M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
,R., Williamson,A., Wohlmann,P. and Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
COMMENT   Contact: Willson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 1556
High quality sequence stops: 249 Source: IMAGE Consortium, LNL This
clone is available royalty-free through LNL ; contact the IMAGE
Consortium (info@image.lnl.gov) for further information.
Insert length: 1556 Std Error: 0.00
Seq primer: -21ml3
High quality sequence stop: 249.
FEATURES
source
Location/Qualifiers
1..380
/organism="Homo sapiens"
/db_xref="GDB:479330"
/db_xref="taxon:9606"
/clone="IMAGE:127169"
/clone_1lb="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pTF73D (Pharmacia)
with a modified polylinker. Site_1: Pac I; Site_2: Eco RI;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
15' AACCTGCAGCAATTAATTAAGAAGCTTTTCTTTTTTTT 3',
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pTF73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Facima Bonaldo."
BASE COUNT 111 a 73 c 86 g 109 t 1 others
ORIGIN
Query Match 80.0%; Score 14.4; DB 10; Length 380;
Best Local Similarity 72.2%; Pred. No. 1.6e+03;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAYTGCGTAAVGTNATH 18
||:||||| ||:|| |::
Db 227 AAYTGCGTGAATGTCATC 210
RESULT 4
A0154673 487 bp DNA linear GSS 16-OCT-1998
A0154673/c HS_3021_A1-C08-T7 CIT Approved Human Genomic Sperm Library D Homo
sapient genomic clone Plate=3021 Col=15 Row=E, DNA sequence.
```

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 00:13:07 ; Search time 2591.91 Seconds  
(without alignments)  
93.732 Million cell updates/sec

Title: US-09-724-841-9  
Perfect score: 18  
Sequence: 1 AAYTGGTNAATGATNATH 18

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	14.4	80.0	174	9	AM880392 QV0-OT003
C 2	14.4	80.0	359	10	BE315807
C 3	14.4	80.0	380	10	R08151
C 4	14.4	80.0	487	12	AO154673 HS_3021_A
C 5	14.4	80.0	490	12	AO132420 HS_3021_A
C 6	14.4	80.0	509	9	AA463370
C 7	14.4	80.0	515	10	BF650545
C 8	14.4	80.0	547	12	TA241H020
C 9	14.4	80.0	550	9	AM688129
C 10	14.4	80.0	566	12	AO421826
C 11	14.4	80.0	584	10	BC082266
C 12	14.4	80.0	600	12	AO947440
C 13	14.4	80.0	609	12	BH098364
C 14	14.4	80.0	654	12	AO329420
C 15	14.4	80.0	674	10	BF645513
C 16	14.4	80.0	700	10	BI271747
C 17	14.4	80.0	709	12	A2192227

18	14.4	80.0	765	12	AO859203	AO859203 nbe0011B
19	14.4	80.0	800	10	BC184658	BC184658 RST3720_A
20	14.4	80.0	838	10	BC069247	BC069247 H3074C12
21	14.4	80.0	872	10	BI758686	BI758686 603024240
22	14.4	80.0	982	9	AL548180	AL548180 AL548180
23	14.4	80.0	994	9	AL572832	AL572832 AL572832
24	14.2	78.9	304	9	BA443796	BA443796 BA443796
25	14.2	78.9	393	12	AO990526	AO990526 Rfc01314
26	14.2	78.9	453	10	N40459	N40459 yv47e01.81
27	14.2	78.9	518	12	AO408665	AO408665 HS_5102_B
28	14.2	78.9	534	9	AI070145	AI070145 UT-R-Y0-1
29	14.2	78.9	566	12	AO991586	AO991586 Rfc02580
30	14.2	78.9	668	12	BS06964	BS06964 BS06964
31	14.2	78.9	689	12	AO990859	AO990859 Rfc01695
32	14.2	78.9	708	9	AV735264	AV735264 AV735264
33	14.2	78.9	735	12	AG029269	AG029269 Pan t10g1
34	14.2	78.9	780	9	BE038814	BE038814 AB07C01_A
35	14.2	78.9	811	10	BC482190	BC482190 602526710
36	14.2	78.9	853	10	BE732877	BE732877 601567811
37	14.2	78.9	890	10	BF626046	BF626046 HV_CBA000
38	14.2	78.9	921	12	CNS03020	AL222909 Tetradon
39	13.4	74.4	123	9	AA559533	AA559533 MC070525
40	13.4	74.4	127	10	N25392	N25392 EST000062_S
41	13.4	74.4	140	9	AA931025	AA931025 SWTBADA00
42	13.4	74.4	140	10	H63019	H63019 EST000185_S
43	13.4	74.4	228	9	AM080888	AM080888 xc38b07_x
44	13.4	74.4	248	9	AA185820	AA185820 MAAD0147
45	13.4	74.4	249	9	AA140564	AA140564 MEG0224

#### ALIGNMENTS

RESULT 1  
LOCUS AM880392 174 bp mRNA linear EST 23-MAY-2000  
DEFINITION QV0-OT0030-100400-188-a05 OT0030 Homo sapiens CDNA, mRNA sequence.  
ACCESSION AM880392  
VERSION AM880392.1 GI:8042402  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE  
AUTHORS 1 (bases 1 to 174)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare  
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

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sequence tags  
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source This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-QV0-OT0030-100  
400-188-a05&tl=2000-04-10&tl=1)  
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